

STIC Search Report Biotech-Chem Library

STIC Database transmission

TO: Minh-Tam Davis

Location: REM-3A24&3C18

Art Unit: 1642

Friday, April 29, 2005

Case Serial Number: 09/674237

From: Toby Port

Location: Biotech-Chem Library

REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Searon Noises

Dear Examiner Davis,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

proty 02/99 04/98



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STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To: Subject: Wednesday, April 27, 2005 12:34 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/674237

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89



----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, April 27, 2005 12:31 PM

To:

Chan, Christina

Subject:

Rush search request for 09/674237

Please search in commercial database, issued patent files, and PGPUB:

1) A nucleotide sequence encoding SEQ ID NO:3, with size limitation of the sequences in the database 100 nucleotides or less.

2) SEQ ID NO:1, with size limitation of the sequences in the database 100 nucleotides or less. 3) SEQ ID NO:2, with size limitation of the sequences in the database 100 nucleotides or less.

Thank you. MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

******	**********
TAFF USE ONLY	Type of Search
earcher:	NA#: AA#:
earcher Phone: 2-	Interference: SPI
ate Searcher Picked up:	S/L:Oligomer:
ate Completed:	Encode/Transl:
earcher Prep/Rev. Time:	Structure#: Te
Online Time:	Inventor: Litigation

endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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AX039313 Sequence
AX039522 Sequence
AX039522 Sequence
AX039312 Sequence
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AX039312 Sequence
AX039513 Sequence
CQ080578 Sequence
CQ114850 Sequence
CQ153723 Sequence
CQ153723 Sequence
CQ154588 Sequence
CQ236983 Sequence
CQ354998 Sequence
CQ374598 Sequence
CQ374898 Sequence
AX035894 Sequence
AX035948 Sequence
AX03384 Sequence
AX039314 Sequence
AX03933 Sequence

Synthetic

Synthetic

Synthetic Sequence

Run on:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonuclectide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 27224 07-FEB-2002;
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1.3%; Score 65; DB 6; L.
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 65; Conservative 0; Mismatches 0;
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Sequence 27224 from Patent WO0210449.
CQ557589.1 GI:41524016
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CQ531908
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/mol_type="unassigned DNA"
/db xref="taxon:10090"
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CQ080578
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BD270480 Synthetic
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                                                                 April 28, 2005, 06:15:47 ; Search time 21159.3 Seconds (without alignments) 11642.487 Million cell updates/sec
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       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                             nucleic search, using sw model
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Maximum Match 100%
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length: 100
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VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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linear PAT 18-NOV-2000
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synthetic construct
other sequences artificial sequences.
other sequences artificial sequences.
1 (bases 1 to 98)
E lawson, A.D.G. and Finney, H.M.
Synthetic transmembrane components
Dynthetic transmembrane components
Artificial Sequence
P THERAPEUTICS LTD
OS Artificial Sequence
PP 17-APR-2000
PP 17-APR-1999
PP 18-APR-1999
PP 18-APR-1
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/organism='Artificial Sequence'
Location/Qualifiers
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A method of altering the properties of a membra
in by substitution of the transmembrane domain
Patent: WO 0063373-A 9 26-CCT-2000;
CELLTECH THERAPBUTICS LIMITED (GB)
LOCATION/QUALIFIERS
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68.2%; Pred. No. 2.1e+02;
tive 0; Mismatches 27;
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/mol type="unassigned DNA"
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/nore="B6463"
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/mol_type="genomic DNA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                                                                                              Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting ma transcripts and splice variants that populate a transcriptome patent: WO 021049-A 1543 07-FEB-2002;
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88.3%; Pred. No. 4.9;
live 0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1. .65
.forganism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 54; DB 6;
98.5%; Pred. No. 0.31;
tive 0; Mismatches
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Synthetic transmembrane components.
BD270475
BD270475.1 GI:33080243
JP 2002541845-A/9.
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/db_xref="taxon:9606"
                                                          Rattus norvegicus (Norway rat)
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Location/Qualifiers
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Location/Qualifiers
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CQ541131.1 GI:41507395
                    GI:41498172
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                                                                                                          Rattus norvegicus
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Best Local Similarity
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                       CQ531908.1
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SOURCE ORGANISM

REFERENCE AUTHORS

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1444 GAGCGCCAGGAGCCAGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503
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                                     1. .100
/organism='Artificial Sequence'.
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A method of altering the properties of a membra in by substitution of the transmembrane domain perent: WO 0063373-A 10. Se-OCT-2000; CELLIECH THERAPRUTICS LIMITED (GB)
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1. 100
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="B6464"
                      Location/Qualifiers

    100
    organism="synthetic construct"

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other sequences, artificial sequences.
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AX039518
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                                                                                                                            /mol_type="genomic DNA"
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                    53
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PR 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908818.9
ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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/organism="synthetic construct"
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Synchetic transmembrane components
Patent: JP 2002541845-A 10 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/10
PD 10-DEC-2002
                                                                                                                                                                                                  DNA
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1 (bases 1 to 100)
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Patent: WO 0063374-A 9 26-CCT-2000
CELITECH THERAPEUTICS LIMITED (GB)
LOCATION/QUALIFIERS
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AX039517
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Best Local Similarity 68.2%;
Matches 58; Conservative (
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PC C1
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BD270476
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PAT 18-NOV-2000

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1437 AGAGCGGGAGCGCCAGCAGCAGGAGCCCAAGCGGCAGCTGGAGCAGAAGCAGCTGGA 1496
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A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain patent: WO 0063373-A 11 26-OCT-2000;
CELLIECH THERAPEUTICS LIMITED (GB)
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0.8%; Score 40.4; DB 6;
Best Local Similarity 71.6%; Pred. No. 4.3e+02;
Matches 53; Conservative 0; Mismatches 21;
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/noce="B6465"

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    /organism="synthetic construct"
/mol_type="unassigned DNA"
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Patent: WO 0063374-A 11 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
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Sequence 11 from Patent WO0063373.
AX039310
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AX039519
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A61P37/06, A61P37/08, C07K14/705, C12N1/15, C12N1/19, C12N1/21, PC
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ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC
CI2N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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                                                                                                                                                                                                                                   27; Indels
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Synthetic transmembrane components
Patent: WO 0063374-A 10 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
1. .100
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Patent: JP 2002541845-A 11 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/11
PP 10-DEC-2002
PF 17-APR-2000 JP 2006612453
PR 16-APR-1999 GB 9908816.3,16-APR-19
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Pred. No. 2.1e+02;
0; Mismatches 27;
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1 (bases 1 to 92)
Lawson, A.D.G. and Finney, H.M.
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Best Local Similarity 68.2%;
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PC A61P17
PC A61P37
C12N5/10,
PC A61P37
C12N5/10,
PC C12N15
FH Key
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PAT 18-NOV-2000

linear

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                                                                                                            Query Match 0.8%; Score 40.4; DB 6; Length 9 Best Local Similarity 71.6%; Pred. No. 4.3e+02; Matches 53; Conservative 0; Mismatches 21; Indels
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/noTe="86466"
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synthetic construct
other sequences; artificial sequences.
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Synthetic transmembrane components
Patent: W0 0063374-A 12 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
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Sequence 12 from Patent WO0063374.
AX039520
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Job time: 21164.3 secs
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A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain patent: WO 0063373-A 12 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
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PR 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908818.9
ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC
C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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Location/Qualifiers
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Patent: JP 2002541845-A 12 10-DEC-2002;
CELLIECH THERAPEUTICS LTD
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                                                                                   Synthetic transmembrane components.
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JP 2002541845-A/12
10-DEC-2002
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April 28, 2005, 05:12:48; Search time 2462.18 Seconds (without alignments) 12223.299 Million cell updates/sec

US-09-674-237B-1

Perfect score:

1 cggcacgaggaggagtggag........gagaattcgatatcaagctt 5084 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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4530610 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 100 Minimum DB 8 Maximum DB 8

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

16Dec04:* geneseqn1980s:* Genesed Database

geneseqn2003cs:* geneseqn2003ds:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2001as:* geneseqn2001bs: geneseqn1990s:* geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2004as:* genesegn2004bs:*

Aac65405 Oligonucl Abk89299 Trinucleo Aac65407 Oligonucl Ac65407 Oligonucl Ac46332 Clone #8 Aav17232 SCA2 gene Aav17233 SCA2 gene Aav17233 SCA2 gene Ad331430 Human gen Aac65409 Oligonucl Aad30431 29 mer ol Aav17231 SCA2 gene Adp49483 Oligonucl Abn54476 Mouse spl Abn28795 Rat splic Adc16446 Short int Adc16445 Short int ac65404 Oligonucl Rat splic Aav17231 SCA2 gene Aac65408 Oligonucl Abn38018 Human spl Description Aac65404 SUMMARIES ADC16446 ADC16445 AAC65404 AAC65405 ABK89299 AAC65406 AAC65407 ACD94308 AAV68382 AAV17233 ADS31430 AAC65409 AAD30431 AAV17231 AAC65408 ADP49483 ABN38018 AAV17232 a DB Query Match Length 69 88 87 78 86 48.8 42.8 41.8 36.6 36.4 35.8 41 40.4 40.4 39.2 39 37.6 Score Result 14 11 11 11 11 11 11 11 12 13 ŝ υ

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22 33.4 0.7 75 24 33.4 0.7 93 25 33.4 0.7 93 26 33.4 0.7 93 27 33.4 0.7 93 28 33.4 0.7 93 31 32.4 0.7 93 32 32.4 0.6 69 33 32.2 0.6 69 34 31.2 0.6 69 36 31.4 0.6 77 37 31.2 0.6 69 38 30.8 0.6 69 40 30.4 0.6 99 41 30.4 0.6 99 42 29.8 0.6 98	AAV17230	AAI26445	ABA74544	AAI55023	ABA39360	AAK49188	AAK23011	ABS48832	ABS22756	AAT78908	AAV17234	3 ADQ95148	ADS31429	AAC65410	AAC65411		·	2 ACH84145	AAV27572		4	AAI84741	•	2 ACH89027	AAX88107
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ALIGNMENTS

BP. RESULT 1 ADP49483

ADP49483 standard; DNA; 80

(first entry) 12-AUG-2004

ADP49483;

Oligonucleotide array related rat oligonucleotide probe No 99.

oligonucleotide array; orthologue; homology; expression distribution; change; gene-expression; rat; probe; ss.

Rattus norvegicus.

JP2004016070-A.

22-JAN-2004

14-JUN-2002; 2002JP-00174208.

14-JUN-2002; 2002JP-00174208.

(HITA) HITACHI LTD.

WPI; 2004-113862/12

Oligonucleotide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonucleotides derived from ortholog gene of different organism immobilized on support.

Disclosure; Page 16; 56pp; Japanese.

The invention relates to a novel oligonucleotide array comprising a number of oligonucleotides derived from an orthologue gene of a different organism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different organisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the orthologue gene of the organism A and organism B. The sequence match degree of the organism species A and the organism species B is less than 70%. The sequence homology of the genes other than the orthologue gene of

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the organism species A and the organism species B is the level-of-
statistical-significance value, calculated using the homology searching
algorithm: basic local alignment search tool (BLAST) and the value is 0.1

or more. The found value or the calculated value of the melting-
temperature of the variant genes other than the orthologue gene of the

organism species A and the organism species B is 20 degrees C or more.

The oligonucleotide array is useful for measuring expression distribution
of the orthologue gene in different organisms. The method is useful for
comparing expression change of the orthologue gene with respect to

comparing expression and for comparing change of the function of
the orthologue gene in different organisms. The oligonucleotide array has
the ability to perform a measurement of gene-expression distribution of
two or more types of organism simultaneously. The oligonucleotide array
improves reliability of measurement. This polynucleotide sequence
represents a probe of a rat gene for comparison against a human gene used
in the oligonucleotide array of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                            1 AGACAIGTGGTGGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTCCCCAAGTTTACGT
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse spliced transcript detection oligonucleotide SEQ ID NO:27224.
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0
                                                                                                                                                                                                                                                                                                                        Score 80; DB 12; Length 80;
Pred. No. 2.7e-09;
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                                                                                                                                                                                                                                                                                         Sequence 80 BP; 19 A; 15 C; 25 G; 21 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No.
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02-MAY-2001; 2001US-0287724P.
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                                                                                                                                                                                                                                                                                                                                                             80; Conservative
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
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The present invention describes oligomucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several

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coligonucleotides, each capable of hybridising selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profilling studies, in qualitatively or
cuantitatively characterising the corresponding transcriptome, and in
cetecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini
libraries to detect transcripts of a sub-transcriptome under a particular
constitution of the libraries may also be used as specialised mini
libraries to detect transcripts of a sub-transcriptome under a particular
constitution appropriate state, and so allowing the detection of tissue
and pathology-specific genes such as those genes only expressed in
specific tissue under a specific pathological condition; to detect
constitution a production genes such as those genes only expressed in
specific apens; and to detect RNA transcriptom
constitution of a transcriptome of a patient suffering from a particular
character and mice, which are used in the exemplification of the
pareent invention. NB. The sequence data for this patent did not form
constitute the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65 BP; 14 A; 14 C; 17 G; 20 T; 0 U; 0 Other;
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1.2e-05;
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100.0%; Pred. No. 1.2
tive 0; Mismatches
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02-MAY-2001; 2001US-0287724P.
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ses 65; Conserv
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Example 1; SEQ ID NO 10766; 47pp; English.

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CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple cranscription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or carriettively characterialism the corresponding transcriptom, and in detecting RNA transcripts and splice variants of human or animal conscriptomes. The libraries may also be used as specialised minical libraries to detect transcripts of a sub-transcriptome under a particular collibraries to detect transcripts of a sub-transcriptome under a particular collogical or pathological state, and so allowing the detection of tissue specific tissue under a specific pathological condition; to detect or pathology-specific pathological condition; to detect condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular collogoner. ABN27253 to ABN59589 represent oligonucleotide sequences from cracs, humans and mice, which are used in the exemplification of the printed specification, but was obtained in electronic format collogonal action, the printed specification, but was obtained in all or premate and so 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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4056 GAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAGTCACTGCGTG 4115 1 GAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAGTC-CTGCGTG 59 1; Gaps Score 54; DB 6; Length 65; Pred. No. 0.0058; 0; Mismatches 0; Indels Sequence 65 BP; 14 A; 13 C; 18 G; 20 T; 0 U; 0 Other; 1.1%; 65; Conservative CAGAGG 4121 Similarity CAGAGG 65 4116 Query Match 9 Local Matches ઠ 셤 δ a

ABN38018 standard; DNA; 60 BP. (first entry) Homo sapiens 15-JUL-2002 ABN38018; RESULT

Human spliced transcript detection oligonucleotide SEQ ID NO:10766. Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant; transcriptome, oligonucleotide library; ss.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

Faigler S; Mintz L, Mintz E, Shoshan A, Wasserman A, WPI; 2002-257383/30.

៧ New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse

Parrish S, Mousses S; Alton EW, Griesenbach U;

Morgan RA, Fire A, O, Cornelison JR,

Caplen NJ, Mor Kallioniemi O,

WPI; 2003-248169/24.

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several circulation units that populate a genome. The library comprises several coligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptom, and in detecting RNA transcripts and splice variants of human or animal contraints to detect transcripte and splice variants of human or animal colibraries to detect transcripte of a sub-transcriptom under a particular biological or pathological state, and so allowing the detection of tissue can pathology-specific genes such as those genes only expressed in the pathology-specific genes such as those genes only expressed in correspondental specific genes; and to detect RNA transcriptom of a transcriptome of a patient suffering from a particular clasuate and specific pathology-specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular content of a transcriptome of a patient suffering from a particular content of a transcriptome of a persent oligonucleotide sequences from human and splice when the such as those genes and splice of the suffering from a particular content of the such was the such as those sense and splice of the such as t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-0308640P.
08-APR-2002; 2002US-0370970P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003012052-A2.
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Matches
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THE STATE OF THE S
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inhibition of expression of a target gene, where (1) comprises double granded RNA of 15-40 nucleotides in length and a 3 or 5 overhang having a length of ornacleotide to 5-nucleotides on each strand, where the baying a length of ornacleotide to 5-nucleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (1); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNAs; (3) an array-based method of assessing a different double-stranded RNAs; (3) an array-based method of assessing a validating a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene comprising any of 311 20-78 nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, and can be used in gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene. They are useful for thereforms
genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene.
                                                                                                                                                                                   present invention describes an RNA (I) used for the interference or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a target gene. They are useful for treating proliferative diseases,
                                                                                                                      Claim 71; SEQ ID NO 171; 176pp; English.
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1445 AGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1504 0.8%; Score 42.8; DB 10; Length 81; 22; Indels Sequence 81 BP; 0 A; 27 C; 27 G; 0 T; 27 U; 0 Other; Pred. No. 3.6; 0; Mismatches 1505 GGGAGCTGGAGCGGCAGC 1522 20 AGCAGCAGCAGCAGC 3 71.8%; 56; Conservative Similarity Query Match Local Matches 용 ð 셤 à

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21

Short interfering double-stranded RNA oligonucleotide SEQ ID NO:170. expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds ADC16445 standard; RNA; 81 BP (first entry) WOZ003012052-A2 18-DEC-2003 Synthetic ADC16445; RESULT 6

Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S; Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U; (USSH) US DEPT HEALTH & HUMAN SERVICES. (CARN-) CARNEGIE INST WASHINGTON. (IMCO-). IMPERIAL COLLEGE INNOVATIONS LTD. 30-JUL-2001; 2001US-0308640P 08-APR-2002; 2002US-0370970P

30-JUL-2002; 2002WO-US024226

13-FEB-2003.

1445 AGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1504 inhibition of expression of a target gene, where (1) comprises double stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang having a length of 0-nucleotides in length and a 3' or 5' overhang having a length of 0-nucleotides in length and a 3' or 5' overhang the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (1); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNA; (3) an array-based method of assessing a phenotypic effect of a double-stranded RNA on a target gene; (4) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interference in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene comprising any of 311 20-78 nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic sectivity, and can be used in gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene. They are useful for treating proliferative diseases, New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression 61 present invention describes an RNA (I) used for the interference or Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; ö Length 81; Oligonucleotide B6463 for chimeric receptor construction. Indels cystic fibrosis; sickle cell anaemia; psoriasis; e sclerosis; organ transplant rejection; diabetes Sequence 81 BP; 27 A; 27 C; 27 G; 0 T; 0 U; 0 Other; 22; Score 42.8; DB 10; Pred. No. 3.6; 0; Mismatches Claim 71; SEQ ID NO 170; 176pp; English 1505 GGGAGCTGGAGCGGCAGC 1522 17-APR-2000; 2000WO-GB001471. 0.8%; 71.8%; 62 AGCAGCAGCAGCAGCAGC AAC65404 standard; DNA; 98 14-FEB-2001 (first entry) eczema; cystic fibrosis; multiple sclerosis; orgar transmembrane domain; ss. Conservative WPI; 2003-248169/24 Query Match Best Local Similarity Matches 56; Conserv a target gene. 40200063373-A1. e.g. cancer. 26-OCT-2000 AAC65404; AAC65404/c 셤 셤 8 ò

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(CLLT) CELLTECH THERAPEUTICS LTD.

Finney HM, Lawson ADG;

WPI; 2001-015774/02

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anchoring region for transmembrane or membrane anchoring regions that are anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell ansemia), dermatological disorders (e.g. psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/diopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1444 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAAAGCAG 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence was used in the construction of chimeric receptors, properties and level of expression of a membrane-associated protein be altered by substituting a transmembrane region or a membrane-
                                                                                                                                                                                                                          Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.8; DB 4; Length 98; Pred. No. 6.9; 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eczema, cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide B6464 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98 BP; 2 A; 37 C; 25 G; 34 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1504 CGGGAGCTGGAGCGCCAGCGAGAGG 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAGGAGCAGCACCCAAAAG 4
                                                     (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC65405 standard; DNA; 100 BP
  99GB-00008816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Conservative
                                                                                                                   Finney HM, Lawson ADG;
                                                                                                                                                                     WPI; 2001-015774/02.
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Best Local Similarity
Matches 58; Conserv
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16-APR-1999;
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ACC5405
ACC5405
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99GB-00008816

16-APR-1999;

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The properties and level of expression of a membrane-associated procein may be altered by substituting a transmembrane region or a membrane-anchoring region for transmembrane region or a membrane not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. esthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1444 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GAGCAGCAGGAGCAGCAGGAGCAGTAGCAGGAGCAGCAGCAGGAGCAGCAGCAGCAGCAGGAG
                                                                                                                                                                              present sequence was used in the construction of chimeric receptors
Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragile X syndrome; Huntington's disease; myotonic dystrophy; spinal and bulbar muscular atrophy; SBMa; SCA I; Kennedy's disease; spinocerebellar ataxia type I; Friedreich's ataxia; DRPLA; dentatorubara-palidoluysian atrophy; SCA8; SCA12; SCA2; SCA6; SCA7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCA3; Machado-Joseph disease; testicular cancer; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.8; DB 4; Length 1 Pred. No. 7; 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; trinucleotide repeat instability; TNR; cancer; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100 BP; 34 A; 26 C; 38 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1504 CGGGAGCTGGAGCGCCAGCGAGAGG 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 cagcadcadcadcaccaaaad 99
                                                                                                                   Example 2; Fig 3; 47pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 68.2
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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The invention relates to detecting (M1) alterations in trinucleotide repeat (TMR) tract lengths comprising: (i) contacting mammalian cells with a shuttle vector (containing approximately 25 repeats) that enters and replicates in the cells; (ii) recovering the replicated shuttle vector from the cells; (iii) introducing the vector into a yeast cell in the presence of a selection agent or (where the expanded TMR confers a confers resistance to the selective agent or His+ phenotype; and (iv) confers resistance to the selective agent or His+ phenotype; and (iv) celecting yeast cells with the shuttle vector containing TMR tract contextions that survived the presence of the selective agent. Also included is an adaptation of the used to detect the contraction of 33 or concern to the present invention are useful for identifying disorders with genetic alterations associated with TMR instability such as cancer espinance rebellar and prostate), Fragile X syndrome, Huntingron's disease, myotonic dystrophy, spinal and bulbar muscular atrophy (SBMA), contactorubaral-palidoluysian atrophy (DRPLA), Friedratch's ataxia and Kennedy's disease. The present sequence is the CAG25 TMR known containing the method of the present sequence is the CAG25 TMR known containing the invantion.
                                                                                                           Detecting alterations in trinucleotide repeat (TNR) tract lengths in mammalian cells useful for identifying disorders associated with TNR instability such as cancer, Fragile X syndrome, Huntington's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75 BP; 25 A; 25 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                        Miret JJ
                                                                                                                                                                                                                                    Example 1; Page 24; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention for expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.6%;
Matches 53; Conservative
                          Pelletier R,
                                                                  WPI; 2002-575460/61
                                                                                                                                                                                       myotonic dystrophy
                        Lahue RS,
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anchoring region for transmembrane or membrane anchoring regions that are anchoring region for transmembrane or membrane anchoring regions that are not naturally part of the protein. The relative response of membrane associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease, cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic psoriasis), neurological disorders (e.g. multiple solerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)

sequence was used in the construction of chimeric receptors

Example 2; Fig 3; 47pp; English

Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.

(CLLT) CELLTECH THERAPEUTICS LTD

Finney HM, Lawson ADG; WPI; 2001-015774/02

99GB-00008816

16-APR-1999;

17-APR-2000; 2000WO-GB001471

of expression of a membrane-associated protein

The properties and level of expression of a membrane-associated protomay be altered by substituting a transmembrane region or a membrane

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1450 CAGGAGCAGGAGCCGAAGCGGCAGCTGGAGAAAGCAGCTGGAGAAAGCAGCAGCAGCAGGAGA 1509
                                                                                   9
                                                                             .
0
Score 41; DB 6; Length 75;
Pred. No. 9.5;
                                20; Indels
                                                                                                                   CIGGAGCGGCAGC 1522
                                                                                                                 1510
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CAGCAGCAGCAGC

61

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1437 AGAGCGGGAGCGCCAAGAAGCCAAAGCGGCAGCTGGAGCTGGAAAGCAGCTGGA 1496

GAAGCAGCGGGAGC 1510

1497

d Š 셤

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GCAGGAGCAGCAGC 13

AAC65407 standard; DNA; 94 BP

RESULT 11 AAC65407 14-FEB-2001 (first entry)

AAC65407;

ö

Gaps

;

Indels

21;

0.8%; Score 40.4; DE 11.6%; Pred. No. 15; ve 0; Mismatches

Local Similarity 71.6%; nes 53; Conservative

Query Match Best Loca Matches

DB 4; Length 92;

Sequence 92 BP; 2 A; 34 C; 24 G; 32 T; 0 U; 0 Other;

27

Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; Oligonucleotide B6465 for chimeric receptor construction. eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; AAC65406 standard; DNA; 92 BP (first entry) transmembrane domain; ss 14-FEB-2001

WO200063373-A1

Synthetic

26-OCT-2000.

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Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; anticathmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; ancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss.
                                                                                 Oligonucleotide B6466 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                              17-APR-2000; 2000WO-GB001471
                                                                                                                                                                                                                                                                     WO200063373-A1.
                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1437 AGAGCGGGAGCGCCAGGAGCAGGCGAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGA 1496
                                                                                                                                                                                                                                                                                                                                                               The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane anchoring region for transmembrane membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 94 BP; 32 A; 25 C; 35 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer cell expressed cDNA #2720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.4; I
Pred. No. 15;
                                                                     (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                           Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACD94308 standard; cDNA; 97 BP.
                       99GB-00008816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 Similarity 71.6%;
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GCAGGAGCAGCAGC
                                                                                                                      Pinney HM, Lawson ADG
                                                                                                                                                                     WPI; 2001-015774/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; ss.
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ACD94308/C
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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing cingle-stranded cDNA by reverse transcribing mRNA with (I), amplifying cond amplifying repse with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleic acid molecule from a genome of an organism; and for sequencing nucleic acid molecule from a genome of an organism; and for sequencing all or part of agenome of an organism; and for sequencing all or part of agenome of an organism mRNA is obtained from mammalian or human cell which is associated with a pathological condition e.g. a colon cancer or bereat cancer cell. The method is useful for analyses of oppulations of subjects and can be used to carry out genetic analyses of large or small populations. further, it can be used to study living an individual or population more or less likely to be afflicted with ciseness such as cancer, to determine antibiotic resistance or nontolect congenital diseases, and the risk of affliction to a foetus, as well as through ove or sperm. The analyses for pathological conditions can be through ove or sperm. The analyses for pathological conditions can be thurbush over sperm. The analyses for pathological conditions can be thus the area of agriculture, for example the genomes of food crops can be thus and the risk of action or present, defects in plant of a plant or determine if resistance can be strided to determine if are example or spenus. Genome can be strided to determine if area can be seed to defermine the cancer or non-particular and the strand of administ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   studied to determine if resistance genes are present, defects in plant genomes can also be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches to therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                           Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Pred. No. 30;
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Matches 59; Conservative 0; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 407; 959pp; English.
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                                                                                                                                                                                                  Simpson AJG, Neto ED,
(SIMP/) SIMPSON A J G. (NETO/) NETO E D.
                                                                                                 BREN/) BRENTANI R R.
                                                                                                                                                                                                                                                                                              WPI; 2003-182626/18.
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Best Local Similarity
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AAV68382/c
ID AAV6831
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AC AAV6831
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CAG

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CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGAG 1509
                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing spinocerebellar ataxis type II - by PCR and determining number of CAG repeat units.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 78;
Pred. No. 53;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCA2 gene CAG repeat unit fragment.
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                                                                                                                                                                                                                                    96WO-JP001999
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Best Local Similarity 67.9%;
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                           Sanpei K;
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                                                                                                                                                                                                                                                                                (SRLS-) SRL INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-1996;
                                                                                                                                                                                             18-JUL-1996;
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                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rsuji S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of a human CAG repeat containing clone DNA sequence isolated using the method of the invention. The method is for analyzhing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CTG repeat and a polymerase and PCR reagants; (b) preparing the nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid with the first and second primers; and (d) detecting the amplified product. The method is used to distinguish between the expression of genes in two or more biological samples, e.g. body fluids, cells, solid tissue or solid and liquid foods. It can be used in medical diagnostics, e.g. to differentiate between normal and diseased tissue or to assess the variation within monozygotic twin pairs. The method allows the isolation and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorace. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441 CGGGAGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAG 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification of differentially expressed genes in various cell type Genome complexity is reduced by the new method which targets genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysing nucleic acid samples - using amplification primers which contain CAG or CTG tri:nucleotide repeats for differential display samples from different sources.
                                                           nucleic acid analysis, variation assessment, neurological disease;
Huntington's chorea; PCR suppression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Clone #8 fragment identified by CAG repeat analysis method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 39; DB 2; Length 89;
llarity 65.5%; Pred. No. 32;
Conservative 0; Mismatches 30; Indels
                                      genome analysis; medical diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 89 BP; 2 A; 23 C; 37 G; 27 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example, Page 32; 44pp; English.
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nes 57; Conserv
                                         repeat; human;
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                                                                                                                                  Homo sapiens
                                                                                                                                                                         WO9849345-A1
                                                                                                                                                                                                                                                             29-APR-1998;
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Best Loc Matches

a 8

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RESULT 14

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AAV1723

BXHXHXB

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0; Gaps

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2 Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;

Query Match

Best Local Similarity 67.9%; Pred. No. 53;

Matches 53; Conservative 0; Mismatches 25; Indels

0; Gaps

1510 CTGGAGCGCCAGCGAGAG 1527
| | | | | | | | | | | 61 CAGCAGCGCCGCCGCG 78

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Search completed: April 28, 2005, 08:43:20 Job time : 2467.18 secs THIS PAGE BLANK (USPTO)

Perfect score:

Seguence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by S' RACE of total RNA from gene trap ES
cell line. BS cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
thtp://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE464
                                                                                                                                                                                                                                                                                                                                                                         CC199586 94 bp mRNA linear GSS 09-MAY-2003
KE464 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
CG572531 OST203191
BH218452 1006078G1
CD497616 Gm Ckr25
AA72619 VUBBbll.r
CR126087 FOrward SC72499 OST203112
AC476761 IMO295B19
BQ234425 h445b08.9
CR147383 Reverse BB0809943 1030014C1
AI316382 uk60a03.y
CV255497 EST883874
D18610 MUSGS01671
CG724316 1119080F0
BE62032 bs11e10.y
BQ234381 h444f06.9
BC624348 h444f06.9
AV674805 AV674805
BQ234381 h444f06.9
AV674805 AV674805
BQ234381 H24650.9
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases, 1 to 94)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell type="Embryonic stem cell"
/clone lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 94; DB 8; Length 94;
100.0%; Pred. No. 2.2e-12;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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/organism="Mus musculus"
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/strain="129 ola"
/db_xref="taxon:10090"
                                                                                                                                AI316382
CV295497
D18610
                                                     CR126087
CG572499
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BQ234483
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Location/Qualifiers
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                               CC199586
CC199586.1 GI:30479626
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Matches 94; Conserv
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AZ448190 IM02477
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AZ804535 ZW0065121
AZ8171347 1M0285121
AZ614077 1M0442B14
BH2255497 1006126F0
BH225549 1006126F0
BH225549 1006126G0
CR272899 Porward B
CR26426 Reverse B
AZ77622 ZW0016114
AQ988931 ZGA1A04NE
CG565168 OST189766
CG340475 NISC 1204
CV030123 9138—Full
                                                                                        April 28, 2005, 06:48:09 ; Search time 15136.1 Seconds (without alignments) 12785.281 Million cell updates/sec
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CO755195 Mdfrt3048
CK459729 929944 MA
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score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
                                                                                                                                                                        1 cggcacgaggaggagtggag......gagaattcgatatcaagctt 5084
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                        34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                nucleic search, using sw model
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AZ804535
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AZ779622
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Maximum Match 100%
Listing first 45 sv
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5084
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gb_htc::
gb_htc::
gb_est3::
gb_est5::
gb_est6::
gb_est6::
gb_gs81::
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Maximum DB seq length: 100
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36.2 36.2 36.2 36.2 36.2 36.2 36.2

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Result Š. 35.6 35.4 34.2 34.2

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GSS 29-MAY-1997

DEFINITION

RESULT 2 AA589590

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ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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983 GTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCTTCAA 1042
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XG352 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
1 (Dases 1 to 46)
                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 64)
Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E.

Cloning of 559 potential exons of genes of human chromosome 21 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: BayGenomics Management (BayGenomics)
Bay Area Functional Genomics Consortium (BayGenomics)
Bay Area Functional Genomics cost.
Sequence tay generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCCCCAAGCAAGAACTATTCTTATGNAGTCAAGTTTACCACAGGCTCAGNTGGNTTCAA
  HSMC18D03 64 bp DNA linear GSS 29-Mi
H.8apiens DNA for trapped exon (ID HMC18D03), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen, H.M., Rossier, C., Chrast, R. and Antonarakis, S.E. Cloning of trapped exons from human chromosome 21 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 64;
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1.1%; Score 54.6; DB 9;
Best Local Similarity 89.1%; Pred. No. 0.021;
Matches 57; Conservative 0; Mismatches 7;
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Genome Res. 6 (8), 747-760 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="trapped exon"
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Unpublished (2001)
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                                                                                                            X88324.1 GI:1437729
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOIR (Kanawycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Whole skin from Il week old CSTBL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                EST 16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 79)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                           AA589590
79 bp mRNA linear EST 16-SEP-1997
4496099:18 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:975568 3' similar to SW:YEJ4 YEAST P43603 HYPOTHETICAL 40.4
KD PROTEIN IN PES4-HIS2 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This Glone is available royalty-free through LLNL, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:556296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3261 TGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
61 PACAGCCACGACAAACTATGAGTGGACACTTAA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:975568"
/sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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ADTITION

FEATURES

Best Loc Matches

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RESULT 3 HSMC18D03

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Gaps

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/sex="Male"
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Unpublished (2000)
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ORGANISM
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AZ448190
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information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 92)
1 (ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MACIBED BY DNA linear GSS 16-FEB-200 2M0032E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0032E18 F, genomic survey sequence. AZ786638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone lib="Mouse 10kb plasmid UUGCNM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                  /cell type="Embryonic stem cell"
/clone lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 46; DB 8; Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                              organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC2M0032E18"
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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Location/Qualifiers
                                                                                                         Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="129 ola"
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Mus musculus
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Plate: 0032 row: E c
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Unpublished (2000)
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Fax: 801 585 7177
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AZ786638/c
LOCUS
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ORGANISM
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KEYWORDS
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1513
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Bunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALAMENYU BY DNA linear GSS 04-OCT-200
1M0245A17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0245A17 R, genomic survey sequence.
AZ448190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AGGAGGAGGAGTAGGAGTAGAAGGAGAAGTAGAAGGAGAAGGAGAAGGAGAAGGAAGGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.9%; Score 44; DB 8; Length 92; Best Local Similarity 67.4%; Pred. No. 12; Matches 62; Conservative 0; Mismatches 30; Indels
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 10000 Std Error: (Plate: 0245 row: A column: 17 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0245A17"
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Location/Qualifiers
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Mus musculus
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55; Conservative
Best Local Similarity
                         Matches
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AZ804535
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                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwadv2 (gel #742114|gb|AR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AV533640.1 GI:8693923
EST.
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DNA Res. 7 (3), 175-180 (2000)
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone_lib="Arabidopsis thaliana flower buds Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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  musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 42.8; DB 8; Length 89; 68.6%; Pred. No. 24; indels iive 0; Mismatches 27; Indels
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                         Laboratory Mouse DNA Resource
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Arabidopsis thaliana
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/ecotype="Columbia"
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Best Local Similarity 68.6
Matches 59; Conservative
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MEDLINE
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DB 1; Length 86;

0.8%; Score 40.6;

Query Match

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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="wouse 10kb plasmid UUGCIM library"
/clone_lib="wouse 10kb plasmid UUGCIM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
vas blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4712114)gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                                                            1458 GGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCTGGAGAAGCAGCGGGAGCTGGAGCG
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Dunn, D., Aoyagi,A., Barber,M., Bacorn,T., Duval,B., Hamil,C., Islam,H., Longarers,S., Mammoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                 Gaps
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0
                                 Indels
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                                 24;
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Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 21
69.6%; Pred. No. 86; tive 0; Mismatches
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Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0065121"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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Rm. 308, Bic
USA
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Best Local Similarity
Matches 49; Conserv
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84112, USA
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AZ837486/c
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                                                                                                                                                                        1457 AGGAGCCCAAGCGGCAGCTGGAGCAGCAGCTGGAGAAGCAGCAGCGGGAGCTGGAGC 1516
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 71)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone_lib="Mouse_10kb plasmid UGGIM library"
/note="Vector: pwD42tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Roose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                         Gaps
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                                                                        DB 8; Length 94;
                                                                                                                      31; Indels
and selected for ampicillin resistance."
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Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: I column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                     Query Match 0.8%; Score 40.4; D
Best Local Similarity 65.6%; Pred. No. 99;
Matches 59; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0285121"
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Location/Qualifiers
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Fax: 801 585 7177
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USA
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AUTHORS
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KEYWORDS
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                            1477 GAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGAGGAGGAGAGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 87)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ837486
2M0132J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0132J14 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Dlasmid inserts of University of Utah Genome Scaffolding with paired end reads from 10kb plasmid inserts
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                             0.7%; Score 36.4; DB 8; Length 71;
llarity 70.0%; Pred. No. 9.5e+02;
Conservative 0; Mismatches 21; Indels
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 0132 row: J column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0132J14"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ837486.1 GI:13007394
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ORIGIN

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrowynamically sheared by repeated passage through a was hydrodynamically sheared to repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pND42 [gi|4732114[gb|AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0442B14R Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0442B14 R, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (Dases 1 to 91)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                             ch 0.7%; Score 36.2; DB 8; Length 87; 1 Similarity 68.5%; Pred. No. 1.1e+03; 50; Conservative 0; Mismatches 23; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: O442 row: B column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/60"
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Location/Qualifiers
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/clone="UUGC1M0442B14"
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 50; Conserv
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ORGANISM
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KEYWORDS
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TITLE

COMMENT

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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pMNA2 (gql 4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2001)
Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbordestanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006126 row: 1
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0
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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Stanford University
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BH225497/c
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TITLE
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64.38;
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Matches 54; Conserv
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TITLE
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/dav stage="leaf"
/dab_host="lough"
/dab_host="lough"
/dab_host="lough"
/done lib="lough"
/done lib=
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and B9111, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                            1374 GGAGCAGCACAGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGCAGGAGAG 1433
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Unpublished (2001)
Contact: Walbot V
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1006126G04.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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Tal: 550 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
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                                                                                                                                                                                                                           Length 91;
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Pred. No. 1.3e+03;
0; Mismatches 30; Indels
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Mol_type="genomic DNA"
Cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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Location/Qualifiers
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BH225515
BH225515.1 GI:16823551
                                                                                                                                                                                                                     0.7%;
Similarity 64.3%;
4; Conservative
                                                                                                                                 ampicillin."
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                                                                                                                                                                                                                                                                                  54;
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Best Local S:
Matches 54
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BH225515/c
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
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0.7%; Score 36; DB 8; Length 91;

Query Match

ORIGIN

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/clone lib="1006 - RescueMu Grid G"
/clone lib="1006 - RescueMu Grid G"
/note="Organ: leaf, Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BgLII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DHIOB
cells were transformed and then screened on LB plates with
                              ö
                                                                                   1374 GGAGCAGCAGCACAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCCGAGCAGGAGAG 1433
                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 08-NOV-2001
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Contact: Walbot Wood Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                           56
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1006126H07.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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                              Gaps
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Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006126 row: 1
Class: transposon-tagged.
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
Pred. No. 1.3e+03;
0; Mismatches 30; Indels
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64.3%; Pred. No. 1.3e+03;
iive 0; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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/organism="Zea mays"
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/dev_stage="adult"
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                           54; Conservative
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QY 1525 GAGGAGGAGGAAGAAGATCGAGAGG 1554

Db 35 AACAGGAAGAGGAAGAGGAAGAGGAAGAGGA

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Search completed: April 29, 2005, 02:01:57 Job time : 15142.1 secs

Query Match 0.7%; Score 35.6; DB 9; Length 96; Best Local Similarity 62.2%; Pred. No. 1.7e+03; Matches 56; Conservative 0; Mismatches 34; Indels

0; Gaps

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RESULT 2
US-09-573-080A-463

Sequence 463, Application US/09573080A

Sequence 463, Application US/09573080A

GENERAL INFORMATION:
SENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATINE THE REPREBUCE:
CURRENT APPLICATION NUMBER: US/09/573,080A

CURRENT FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 463

LENGTH: 69
                                                                                                                                                                                                                                                                                    US-09-043-303-12
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Sequence 11, Appl
Sequence 10, Appl
Sequence 13, Appl
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26, Appl
                                                                           April 28, 2005, 07:02:07 ; Search time 760.328 Seconds (without alignments) 10941.112 Million cell updates/sec
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: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/packfiles1.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-573-080A-463
US-09-043-303-11
US-09-043-303-11
US-09-043-303-13
US-09-573-080A-462
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US-08-56-978B-24
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US-08-56-978B-24
US-08-56-978B-24
US-08-13-399C-14585
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US-07-812-421-25
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US-08-823-771-57
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US-09-281-481A-7
US-09-513-999C-35527
US-09-513-999C-29269
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length
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seq length: 100
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Sequence 12, Application US/09043303

Patent No. 6251589

GENERAL INFORMATION:
APPLICANT: TSUJI, Shoji

TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Piteners Therefor
FILE REFERENCE: 0760-0341P

CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT PILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: PCT/JP96/01999

EARLIER PILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 12

LENGTH: 78
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US-08-707-237A-29
US-08-402-085B-58
US-08-475-411A-25
US-08-478-029A-25
US-09-444-791A-58
US-09-573-080A-468
US-08-182-175A-89
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US-08-175-155-23
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al Similarity 67.9%;
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ORGANISM: Homo sapiens
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0.6%; Score 32.2;
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Best Local Similarity 73.73
Matches 42; Conservative
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LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                   ) OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in CTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari; OTHER INFORMATION: able and is often polymorphi
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APPLICANT: TSUJI, Shoji
APPLICANT: TSUJI, SANDEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER FILING DATE: 1998-05-18
EARLIER FILING DATE: 1996-07-18
SAUGHER PER SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STANDEI, Kazujiro
APPLICANT: SANDEI, Kazujiro
APPLICANT: SANDEI, Kazujiro
APPLICANT: SANDEI, Kazujiro
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                            DB 4; Length 69;
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66.7%; Pred. No. 11;
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Patent No. 6251589
GENERAL INFORMATION:
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US-09-043-303-11
Sequence 11, Application US/09043303
Patent No. 6251589
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Best Local Similarity 72.1%;
Matches 49; Conservative
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Best Local Similarity 66.7
Matches 52; Conservative
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CRGANISM: Homo sapiens
US-09-043-303-11
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                                               ORGANISM: Artificial FEATURE:
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SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN
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US-09-573-080A-462
                                                                                                            1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TSUJI, Shoji
APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER PLING DATE: 1996-07-18
NUMBER OF SEO ID NOS: 17
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Query Match 0.7%; Score 34; DB 3; Length 75; Best Local Similarity 66.2%; Pred. No. 47; Matches 49; Conservative 0; Mismatches 25; Indels
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Sequence 462, Application US/09573080A

FALCHI WO. 6828097

GENERAL INFORMATION:

APPLICANT: ROGAN, KNOLL

APPLICANT: ROGAN, PETER

FILE OF INVENTION: SINGLE COPY GENOMI

FILE REFERENCE: 30307
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; Sequence 13, Application US/09043303
; Patent No. 6751589
; GENERAL INFORMATION:
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DB 4; Length 69;

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RESULT 9
US-08-556-978B-24
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                                                                     1476 GGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGAGCTGGAGCGCCAGCGAGGAGGAGAAG 1535
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                                                                                                           81 GCGGCCGCTGGAGCTGGAGCAGGAGCCGAGATCACCACGGGTGCTGGAGCAGGAAGGGAC 22
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                                                                                                                                                                                                                                                                                                              Sequence 4823, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburset al.
TITLE OF INVENTION: Wileic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE NOT INVENTION: Nuclear caids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20105
LENGTH: 89
                            Gaps
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Pred. No. 2.6e+02;
0; Mismatches 31; Indels
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Pred. No. 2.6e+02;
0; Mismatches 31; Indels
                          23; Indels
  66.7%; Pred. No. 1.3e+02;
tive 0; Mismatches 23
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8-09-270-767-20105/c
; Sequence 20105, Application US/09270767
; Patent No. 6703491
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ORGANISM: Drosophila melanogaster
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; ORGANISM: Drosophila melanogaster
US-09-270-767-20105
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Best Local Similarity 61.7%;
Matches 50; Conservative (
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Best Local Similarity 61.7%;
Matches 50; Conservative
Best Local Similarity 66.7
Matches 46; Conservative
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LENGTH: 89
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Sequence 24, Application US/08556978B
Patent No. 6268169
GENERAL INPORMATION:
APPLICAMT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPINER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: B. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: B. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: ILMINITON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
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APPLICANT: PAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 30.4; DB 3; 71.4%; Pred. No. 4.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR-9389-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-556-978B-25/c
; Sequence 25, Application US/08556978B
; Patent No. 6268169
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302-773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-556-978B-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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STATE:
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; Sequence 14585, Application US/09513999C; Patent No. 6783961
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                MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic"

US-08-068-747-1
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Best Local Similarity 59.3%;
Matches 48; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: r=a or g
US-09-513-999C-14585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 40
OTHER INFORMATION: n=a,
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
linear
                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-513-999C-14585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David B.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
CORRESSONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATORING NOWN NEW
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.6%; Score 30.4; DB 3; Best Local Similarity 71.4%; Pred. No. 4.9e+02; Matches 40; Conservative 0; Mismatches 16;
                  SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
  OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                            CR-9389-A
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TRIECOMMUNICATION INFORMATION:
TRIEPHONE: 617-861-6240
                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILLING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-068-747-1/c; Sequence 1, Application US/08068747; Patent No. 569593; GENERAL INFORMATION:
                                                                                                                                                                                                                          NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA (genomic)
US-08-556-978B-25
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                             i: 93 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusett
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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1465 AAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAAAGCAGCGGGAGCTGGAGCGGCGCAGCGA 1524
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERBYCE: 59.US2.REG
CURRENT FILIAGO DATE: 2000-02-24
FILE REPERBYCE: 59.US2.487
PRIOR PELIAGION NUMBER: US 60/122,487
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SEQ ID NO 14585
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AAGCGGCGTCGCCGCCTGGAGCAGCAGCAGCCGNACGAGCAGCGGAGGCGRTCGGGA 63
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                                                              0; Gaps
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Sequence 26, Application US/07814220

GENERAL INFORMATION:

APPLICANT: Cacced, Thomas

APPLICANT: Toth, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

ITTLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,

STREET: Suite 900
                                                                                                                       1471 CAGCTGGAGCTGGAGAAGCAGCTGGAGGAGCAGCGGGAGCTGGAGCGGCAG 1521
                                                                                                                                                                               Query Match 0.6%; Score 30.2; DB 1; Length 51; Best Local Similarity 74.5%; Pred. No. 3.7e+02; Matches 38; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 4; Length 86;
Pred. No. 6e+02;
1; Mismatches 32; Indels
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.тhев 32; Indels
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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/07814220 Patent No. 5925540
                      NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2210
TELEFAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other nucleic
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SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         INFORMATION FOR SEG ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-391-9035
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CITY: Reston
STATE: VA
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-07-814-220-25/c
                                                                                                                                                                                                                                                                                                                                                       US-07-812-421-26
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APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas
APPLICANT: Stumminski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE MITTHAM, CURTIS & WHITHAM
STREET: Rescon Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
0.6%; Score 29.4; DB 2; Length 57;
Best Local Similarity 70.9%; Pred. No. 6.6e+02;
Matches 39; Conservative 0; Mismatches 16; Indels
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTONNEY/AGENT INFORMATION:
AMALICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Restron
STATE: VA
COUTRY: USA
ZD191
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION 1435
PROM APPLICATION NUMBER: US/07/812,421
FILING DATE: 25-DEC-1991
CLASSIFICATION NUMBER: US/07/812,421
FILING DATE: 25-DEC-1991
FILING DATE: 25-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other nucleic acid /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFRENCE/POCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-210
TELEFAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/07812421
Patent No. 5932697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
DESCRIPTION:
                                                             20191
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US-07-812-421-26
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1468 CGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1522
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APPLICANT: Caccei, Thomas
APPLICANT: Toth, Thomas
APPLICANT: Szumanski, Maria B.W.
APPLICANT: Szumanski, Maria B.W.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION NUMBER OF SEQUENCES: 43
CORRESPONDENCES: 43
ADDRESSEE: WHITHAM, CURTIS & WHITHAM STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., STREET: Suite 900
                  Length 57;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
FILING DATE: 23-DEC-1991
FILING DATE: 25-DEC-1991
FILING DATE: 25-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: GIT.016
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      16;
Query Match

0.6%; Score 29.4; DB 2;
Best Local Similarity 70.9%; Pred. No. 6.6e+02;
Matches 39; Conservative 0; Mismatches 16;
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0
Ouery Match 0.6%; Score 29.4; DB 2; Length 62;
Best Local Similarity 70.9%; Pred. No. 6.9e+02;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps
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ò g Search completed: April 29, 2005, 02:23:45 Job time: 762.328 secs

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4058 GCAGTTTACCTCATTTGACCTTAGTTGCATGTGAAAATGTCTGAGTCACTGCGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.3%; Score 65; DB 10; Length 65
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 65; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                      April 28, 2005, 07:33:31; Search time 2706.88 Seconds (without alignments) 11433.739 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \( \cgn2_6 \) ptodata/1 \) pubpna/USO7_PUBCOMB.seq:*

2: \( \cgn2_6 \) ptodata/1 \) pubpna/PCT_RW PUB.seq:*

3: \( \cgn2_6 \) ptodata/1 \) pubpna/USO6_NEW PUB.seq:*

4: \( \cgn2_6 \) ptodata/1 \) pubpna/USO6_NEW PUB.seq:*

5: \( \cgn2_6 \) ptodata/1 \) pubpna/USO6_NEW PUB.seq:*

6: \( \cgn2_6 \) ptodata/1 \) pubpna/USO8_NEW PUB.seq:*

7: \( \cgn2_6 \) ptodata/1 \) pubpna/USO8_NEW PUB.seq:*

8: \( \cgn2_6 \) ptodata/1 \) pubpna/USO8_NEW PUB.seq:*

9: \( \cgn2_6 \) ptodata/1 \) pubpna/USO8_NEW PUB.seq:*

10: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

11: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

12: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

13: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

14: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

15: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

16: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

17: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

18: \( \cgn2_6 \) ptodata/1 \) pubpna/USO9_PUBCOMB.seq:*

19: \( \cgn2_6 \) ptodata/1 \) pubpna/USO10_PUBCOMB.seq:*

19: \( \cgn2_6 \) ptodata/1 \) pubpna/USO10_PUBCOMB.seq:*

10: \( \cgn2_6 \) ptodata/1 \) pubpna/USO10_PUBCOMB.seq:*

11: \( \cgn2_6 \) ptodata/1 \) pubpna/USO10_PUBCOMB.seq:*

12: \( \cgn2_6 \) ptodata/1 \) pubpna/USO10_PUBCOMB.seq:*

22: \( \cgn2_6 \) ptodata/1 \) pubpna/USO0_NEW PUB.seq:*

22: \( \cgn2_6 \) ptodata/1 \) pubpna/USO0_NEW PUB.seq:*

22: \( \cgn2_6 \) ptodata/1 \) pubpna/USO0_NEW PUB.seq:*
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                               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-908-975-10766

US-09-864-867-463

US-10-786-970A-463

US-10-33-894A-6

US-10-407-818-8

US-10-407-818-8

US-10-759-731A-156

US-09-864-867-462

US-09-864-867-462
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM nucleic - nucleic search, using sw model
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                                                            Copyright
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                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                  Title:
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		31.2		77	19	US-10-852-797-339		339. App	
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		30.8		66		US-10-029-386-17340		17340. A	
U		30.4		87		US-10-759-731A-155		155. App	
		30.4		96		US-10-061-201-11		11, Appl	
n 1		29.8		16		US-10-029-386-22222		22222, A	
	19	29.4	9.0	8 5	2:	0 US-09-373-658-52	Sequence	52, Appl	
Ü		20.7		98		US-10-759-88/-32 US-10-759-731A-158		158, App	
N		29.4		97		US-10-023-066A-57		57, Appl	
		29.4	•	97	18	US-10-804-678-57		57, Appl	
		4.0		א ני		US-10-UZ1-323-14338		14338, A	
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		28.8		6	18	US-10-021-323-14335		14335, A	
		28.8		68		US-10-021-323-15706		15706, A	
m		28.6		51	18	US-10-865-478-506		506, App	
e		28.2	•	28		US-10-275-071-15	Sequence 1	15, Appl	
m ·		28.2	•	84		US-10-023-066A-65		55, Appl	
m		28.2		84		US-10-804-678-65		55, Appl	
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71 (9 C		200	2 6	9-854-867-468		168, App	
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υ (20 00	•	ο c	4.	-023-066A-		ob, Appl	
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						ALIGNMENTS			
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RESULT	1								
0-SD	-806-	975-272	24						
, Seq	nence	27224,	Sequence 27224, Application US/0990897	tion	ns/c	39908975			
- A	Licat.	Publication No. USZ	USZODAC	16584	3A1				
	PT.TCA	APPLICANT SHOSHAN	SHAN AVI	7					
	APPLICANT:)	SSERMAN,	Alor					
	PLICAL								
	APPLICANT:		MINTZ, Liat	ת					
	PLICA	NT: FA	FAIGLER, Simchon	imchc	ផ្ត				
T.	TITLE	F INVEN	IO . NOITE	TAPT T	S E	OF INVENTION: OLIGONOCLECTIDE LIBRARY FOR DETECTING RNA	KNA TRANS	TRANSCRIPTS AND S	SPLICE
	LE REI	FERENCE	FILE REFERENCE: 36688-0005	0000	5				
	RRENT	APPLIC	ATION NU	MBER:	us/	CURRENT APPLICATION NUMBER: US/09/908,975			
	RRENT	FILING	CURRENT FILING DATE: 2001	2001-07	07-2	02			
	IOR AL	PPLICAT	ION NUME		35 6C	US 60/287,724			
		ILING D	FILING DATE: 2001-05-02	1-05-	20.5				
	PKIOK A	PPLICAT	PRIOR APPLICATION NUMBER: US 60/	EK:	30 6	7/221,607			
	MBED	DE CEO	FRIOR FILLING DAILS: 2000-0/-	20227	0				
	SOFTWARE	R. Date	nt In ver	יייייייייייייייייייייייייייייייייייייי	~				
S	ID NO	•	27224						
	TYPE: DNA	DNA	. '						
•	RGANIE	SM: Mus	ORGANISM: Mus musculus	10					
60-SD	-806-	975-216	24						

4117 ö

Gaps ö

Length 65;

9

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APPLICANT: USAN, ENDLA H
APPLICANT: GAN, ENDLA H
APPLICANT: ROGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 463, Application US/10786970A

Sequence 463, Application WS/10786970A

Publication NO. 10050064449A1

RPUBLICANT: JOAN, KNOLL

APPLICANT: JOAN, KNOLL

APPLICANT: JOAN, KNOLL

APPLICANT: JOAN, RNOLL

APPLICANT: JOAN, RNOLL

APPLICANT: JOAN, RNOLL

APPLICANT: JOAN, PRIER

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

FILE REFERENCE: 30307

CURRENT APPLICATION NUMBER: US/10/786, 970A

CURRENT PILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SOFTWARE: Patentin version 3.0

SEQ ID NO 463

LENGTH: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many entherial genomes. Length of core repeating element is varioTHER INFORMATION: able and is often polymorphic
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Length 60;
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0.7%; Score 37.6; DB 10; Length
Best Local Similarity 72.1%; Pred. No. 6.6;
Matches 49; Conservative 0; Mismatches 19; Indels
                                              Indels
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0.7%; Score 37.6; DB 19;
Best Local Similarity 72.1%; Pred. No. 6.6;
Matches 49; Conservative 0; Mismatches 19;
  Score 48.8; DB 10;
Pred. No. 0.0039;
0; Mismatches 7;
                                                                                                                                                                                                                                   Sequence 463, Application US/09854867
Publication No. US20030224356A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
      1.0%;
        Query Match
Best Local Similarity 88.3
Matches 53; Conservative
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; Sequence 10766, Application US/09908975
; Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHNAN, Avi
APPLICANT: MINIZ, Eli
APPLICANT: MINIZ, Liat
CURRENT: PAIGNER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REPERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US 60/281,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR APPLICATION NUMBER: US 60/221,607
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10066
LIBRGTH: 60
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ORGANISM: Rattus norvegicus
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Best Local Similarity 98.5
Matches 65; Conservative
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US-09-908-975-10766
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                                     4118 GAGGC 4122
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US-09-908-975-10766
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US-09-908-975-1543
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63;

Length

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Query Match 0.7%;
Best Local Similarity 75.4%;
Matches 43; Conservative
US-10-407-818-8
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                   1455 GCAGGAGGCCAAAGCGGCAGCTGGAGCTGGAAAGCAGCTGGAGAAGCAGCGGGAGCTGGA 1514
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                                                            APPLICANT: RABBANI, BLAZAR
APPLICANT: STAVRIANOPOULOS, JANNIS G.
APPLICANT: STAVRIANOPOULOS, JANNIS G.
APPLICANT: DONGGAN, JAMES J.
TITLE OF INVENTION: MULTISIGNAL LABELING REAGENTS, AND PROCESSES AND USES
TITLE OF INVENTION: THEREFOR
PILE REFERENCE: ENZ-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                              Sequence 6, Application US/10333894A
; Publication No. US20040259085A1
; GENERAL INPORMATION:
; APPLICANT: Chang, Chawnshang
; APPLICANT: Hsing, Ann
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 21108.0001U1
; CURRENT APPLICATION NUMBER: US/10/333,894A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FRASEC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:/note = ; OTHER INFORMATION: synthetic construct
US-10-333-894A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Combined DNA/RNA Molecule: OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.7%; Score 36.6; DB 18; Length EBest Local Similarity 65.1%; Pred. No. 15; Matches 54; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/407,818
CURRENT FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 8
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1510 CTGGAGCGCAGCGAGAGGAGGA 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CAGCAACAGCAGCAACAGCAGCA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10407818; Publication No. US20040198971A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: 3'-amidated
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ORGANISM: Artificial Sequence
                                                                                                            1515 GCGGCAGC 1522
                                                                                                                                                       GCAGCAGC 68
                                                                                                                                                                                                                                                     US-10-333-894A-6
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LENGTH: 87
                                                                                                                                                       61
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                 ö
                                                                                                                                                          1466 AGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1522
                                                                                                                                                                                                                               Gaps
                                                                                     ö
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILLING DATE: 2000-05-04
PRIOR PILLING DATE: 2000-05-05
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-09-04
PRIOR PILLING DATE: 2000-09-04
PRIOR PILLING DATE: 2000-09-07
PRIOR PILLING DATE: 2000-09-07
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING
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INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
INFORMATION: EXPRESSED IN ADILL LIVER, SIGNAL =
INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
Score 34.6; DB 18;
Pred. No. 45;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-864-761-24680/c
; Sequence 24680, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INCRWATION:
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OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN HELLA,
OTHER INFORMATION: EXPRESSED IN HELLA,
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NAME/KEY: misc feature
LOCATION: (50)...(50)
OTHER INFORMATION: y is c or t
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OTHER INFORMATION: s is g or c
                                                LOCATION: (43) ... (43)
OTHER INFORMATION: k is g or t
                                                                                                                       LOCATION: (46)...(46)
OTHER INFORMATION: k is g
                                    WAME/KEY: misc_feature
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                   NAME/KEY: misc feature
LOCATION: (46)..(46)
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US-09-854-867-462
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                                                                                                                                                                                                                           1468 CGGCAGCTGGAGCAGCTGGAGAAGCAGCTGGAGAGCAGCGGGAGCGGCGCAGCGAGA 1526
                                                                                                                                                                                                                                                            Query Match 0.7%; Score 33.4; DB 9; Length 93; Best Local Similarity 72.9%; Pred. No. 1.3e+02; Matches 43; Conservative 0; Mismatches 16; Indels
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN FEARL LIVER, SIGNAL = 4.6

CTHER INFORMATION: NT HIT: gi5031896, EVALUE 2.00e-13

OTHER INFORMATION: BST_HUMAN HIT: R18580.1, EVALUE 3.00e-13

US-09-864-761-24680
                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: VLK ala scan
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NAME/KEY: misc_feature
LOCATION: (37)..(38)
OTHER INFORWATION: s is g or c
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LOCATION: (41)...(41)
OTHER INFORMATION: s is g or c
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: y is c or
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OTHER INFORMATION: y is c
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LOCATION: (28)..(28)
OTHER INFORMATION: s is g
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OTHER INFORMATION: 8 is 9
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OTHER INFORMATION: r is FEATURE:
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LOCATION: (34)..(35)
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1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAAGCAGCTGGAGAAGCAGCGGGAGGAGCTGG 1513
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Best Local Similarity 41.9%; Pred. No. 2.3e+02;
Matches 36; Conservative 22; Mismatches 28;
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LOCATION: (59)..(59)
OTHER INFORMATION: y is c or t
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OTHER INFORMATION: s is g or c
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; OTHER INFORMATION: k is g or t
US-10-759-731A-156
LOCATION: (55)...(55)
OTHER INFORMATION: r is a or g
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THER INFORMATION: s is g or c
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OTHER INFORMATION: y is c or t
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OTHER INFORMATION: m is a or c
                                                                                          LOCATION: (56)..(56)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (61)...(61)
OTHER INFORMATION: r is a or g
                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (58)..(58)
OTHER INFORMATION: k is g
                                                                NAME/KEY: misc feature
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1444 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 339, Application US/10852797
Publication No. US20050064455A1
GENERAL INFORMATION:
APPLICANT: Genomic Health, Inc.
APPLICANT: Miller, Kathy D.
APPLICANT: Miller, Kathy D.
APPLICANT: Sledge, George
APPLICANT: Sledge, George
APPLICANT: Soule, Sharon
TITLE OF INVENTION: Gene Expression Markers for Predicting
TITLE OF INVENTION: Response to Chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                         APPLICANT: GENOMIC HEALTH, INC.
APPLICANT: GENOMIC HEALTH, INC.
APPLICANT: CODICID, Melody
APPLICANT: CODICID, Melody
APPLICANT: Baker, Joffre
APPLICANT: Baker, Joffre
APPLICANT: Baker, Joffre
APPLICANT: BAREN, Steven
APPLICANT: BAREN, STEVENSION MARKERS FOR BREAST
TITLE OF INVENTION: CANCER PROGNOSIS
FILE REFERENCE: 39740/0008 US
CURRENT APPLICATION NUMBER: US/010/758,307
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 60/440,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%; Score 31.2; DB 18; Best Local Similarity 70.0%; Pred. No. 4.7e+02; Matches 42; Conservative 0; Mismatches 18;
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0.6%; Score 31.2; DB 19;
Best Local Similarity 70.0%; Pred. No. 4.7e+02;
Matches '42; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 39740-0010
CURRENT APPLICATION NUMBER: US/10/852,797
CURRENT FILING DATE: 2004-05-24
FRIOR APPLICATION NUMBER: 6/473,970
FRIOR FILING DATE: 2003-05-28
NUMBER OF SEQ ID NOS: 372
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 339
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 77
                                    Sequence 66, Application US/10758307
Publication No. US20040209290A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Amplicon US-10-758-307-66
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                                                                                  GENERAL INFORMATION:
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        US-10-758-307-66
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                                                                         APPLICANT: JOAN, KNOLL H
APPLICANT: JOAN, KNOLL H
APPLICANT: ROGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 462
LENGTH: 69
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Segrible Application US/10786970A

Fublication No. US20050064449A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING CURRENT APPLICATION NUMBER: US/10/786,970A

CURRENT FILING DATE: 2004-02-24

PRIOR APPLICATION NUMBER: US/09/573,080

WUMBER OF SEQ ID NOS: 479

SOFTWARE: Patentin version 3.0

SEQ ID NO 462
                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphic US-09-884-867-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphi
US-10-786-970A-462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 32.2; DB 10; Length 69; Best Local Similarity 66.7%; Pred. No. 2.3e+02; Matches 46; Conservative 0; Mismatches 23; Indels
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Pred. No. 2.3e+02;
0; Mismatches 23; Indels
Sequence 462, Application US/09854867
Publication No. US20030224356A1
GENERAL INFORMATION:
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Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGAGGAGGA 69
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US-10-786-970A-462
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Search completed: April 29, 2005, 03:41:18 Job time: 2708.88 secs
                                                                           1487 AGCAGCTGGAGAAG 1500
                                                                                                                               71 AGGAGAAGGAGAAG 84
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HAZEL, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ACOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                   TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF FILE REFERENCE: GNN-534202 CURRENT APPLICATION NUMBER: US/10/085,906 CURRENT FILING DATE: 2002-02-27 PRIOR APPLICATION NUMBER: US 60/126,215 PRIOR PILING DATE: 1999-03-25 PRIOR PILING DATE: 1999-03-25 PRIOR FILING DATE: 2000-24 PRIOR FILING DATE: 2000-03-24 PRIOR FILING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.6%; Score 31.2; DB 14; Length 86; Best Local Similarity 60.7%; Pred. No. 5e+02; Matches 51; Conservative 0; Mismatches 33; Indels
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8

OTHER INFORMATION: HIT: D86240.2, EVALUE 4.90e+00
US-10-029-386-17340
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174
LENGTH: 86
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; Publication No. US20030194704A1
; GENERAL INFORMATION:
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OTHER INFORMATION: MAP TO AL135920.4
OTHER INFORMATION: EXPRESSED IN BONE
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                                              Sequence 174, Application US/10085906; Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
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ORGANISM: Homo sapiens
US-10-085-906-174
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ORGANISM: Homo sapiens
RESULT 14
US-10-085-906-174/c
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LENGTH: 99
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AX384806 Sequence
BAZ70479 Synthetic
AX039312 Sequence
AX039521 Sequence
AX039521 Sequence
AX225566 Pan trog1
X69669 R.ratus (SAUS)
AX159550 Sequence
CQ114850 Sequence
CQ13678 Sequence
CQ13673 Sequence
CQ13678 Sequence
CQ136983 Sequence
CQ37588 Sequence
CQ31642 Sequence
CQ31642 Sequence
CQ374588 Sequence
CQ374588 Sequence
CQ31642 Sequence
CQ31642 Sequence
AXC3537 Sequence
AXC3537 Sequence
BDZ70481 Synthetic
AXC39314 Sequence
AXC39315 Sequence
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 10766 07-FEB-2002; Compugen Inc. [US)
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1 B270475
1 B270475.1 GI:33080243
JP 2002541845-A/9.
8ynthetic construct
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88.3%; Pred. No. 5.1;
ive 0; Mismatches
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                          AX039521
AY225366
RRGR99
                                                                       AR159550
CQ080578
CQ114850
CQ186430
CQ186430
CQ236983
CQ236983
CQ2348908
CQ311642
CQ348908
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AR159553
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BD270481
AX039314
AX039523
BD270482
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Best Local Similarity
Matches 53; Conserv
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                                                                      April 28, 2005, 06:15:47; Search time 15157.7 Seconds (without alignments) 11642.487 Million cell updates/sec
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Synthetic
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Sequence
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Synthetic
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AJ388053 Hyla chry
AF143273 Vitis vin
BD270480 Synthetic
AX039313 Sequence
AX039522 Sequence
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BD270475 Synthetic
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                                                                                                                                    1 atggetcagtttcccacacc.....tggaccccagccagta 3642
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BD270477
AX039310
AX039519
BD270478
AX039311
AX039520
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AX039517
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                    4708233 segs, 24227607955 residues
                                                                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                    nucleic search, using sw model
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AX039520
AR159552
HCH388053
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AX039309
AX039518
BD270477
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BD270480
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Gapop 10.0 , Gapext 1.0
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90 bitg: *
90 bit: *
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Maximum DB seq length: 100
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11:
12:
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AG1P37/06,AG1P37/08,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
88 GAGCAGCAGGAGCAGCAGCAGCAGTAGCAGAGCAGCAGCAGCAGGAGCAGCAGGAGCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF 17-APR-2000 JP 2000612453
PF 17-APR-2000 JP 2000612453
PR 16-APR-1999 GB 9908818.9
PR 16-APR-1999 GB 9908818.9
ALASTAIR DAVID GRIPPTIMS LAWSON HELENE MARGARET FINNEY PC
C12N15/09, A61K38/00, A61R48/00, A61P1/00, A61P1/06, PC
PC A61P11/00, A61P17/06, A61P19/02, A61P25/00, PC
PC A61P25/00,
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27;
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 100)
Lawson, A.D.G. and Finney, H.M.
Synthetic transmembrane components
Patent: UP 2002541845-A 10 10-DEC-2002;
CELLTECT THERAPEUTICS LTD
OS Artificial Sequence
Pur JP 2002541845-A/10
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1.1%; Score 41.8; DB 6;
Best Local Similarity 68.2%; Pred. No. 2e+02;
Matches 58; Conservative 0; Mismatches 27;
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/db_xref="taxon:32630"
/noTe="B6463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic transmembrane components. BD270476 BD270476.1 GI:33080244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic transmembrane components Patent: WO 0063374-A 9 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB) Location/Qualifiers
                                                                                                                                                                                                                         AX039517 98 bp
Sequence 9 from Patent WO0063374.
AX039517
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                                                       1246 CGGGAGCTGGAGCGCCAGCGAGG 1270
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PC C12N1
CC B6464
FH Key
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TITLE
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JOURNAL
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BD270476
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C12N15/09, AGIK38/00, AGIK48/00, AGIP3/10, AGIP3/10, AGIP7/06, PC
AGIP11/06,
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A method of altering the properties of a membra in by substitution of the transmembrane domain Patent: WO 0063373-A 9 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB)
                                                                        Synthetic transmembrane components
Patent: JP 2002541845-A 9 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/9
PD 10-DEC-2002
PF 17-APR-2000 JP 2000612453
PR 16-APR-1999 GB 9908816.3,16-APR-
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Lawson, A.D.G. and Finney, H.M.
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CLICATE SEQUENCES:

I (bases 1 to 91)

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OS Artificial Sequence

PN JP 2002541845-A11

PD 10-DEC-2002

PR 17-ARR-2000 JP 2006612453

PR 17-ARR-2000 JP 2006612453

PR 17-ARR-2000 JP 2006612453

PR 17-ARR-1999 GB 9908818.9 F

ALASTAIR DAVID GRIFFTTHS LAWSON HELBNE WARGARET FINNEY PC

C12N15/09, A61R93/00, A61R917/06, A61P19/02, A61P25/00, A61P21/06, PC

A61P217/06, A61P25/00,

PC A61P217/06, A61P217/06, A61P19/02, A61P25/00, A61P21/2N1/21,

CANSTAIR DAVID GRIFFTHS LAWSON HELBNE WARGARET FINNEY PC

A61P217/06, A61P217/06, A61P217/06, A61P21/115, C12N1/19, C12N1/21
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/organism='Artificial Sequence'.

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1.1%; Score 41.8; DB 6; Length 1
Best Local Similarity 68.2%; Pred. No. 2e+02;
Matches 58; Conservative 0; Mismatches 27; Indele
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1.1%; Score 41.8; DB 6; Length 100;
Best Local Similarity 68.2%; Pred. No. 2e+02;
Matches 58; Conservative 0; Mismatches 27; Indels
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Matches 58; Conservative 0; Mismatches 27; Indels
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A method of altering the properties of a membra in by substitution of the transmembrane domain beant: WO 0063373-A 10 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB)
                                                                                     /organism="synthetic construct"
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Synthetic transmembrane components
Patent: WO 0063374-A 10 26-OCT-2000;
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1179 AGAGCGGGAGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCAGCAGCAGCTGGA 1238
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PN JP 2002541845-A/12
PD 10-DEC-2002
PP 17-DEC-200 JP 2000612453
PR 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908818
ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC C12N15/09,A61R38/00,A61R48/00,A61R1/00,A61R1/10,A61R7/06,
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/organism='Artificial Sequence'
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A method of altering the properties of a membri
in by substitution of the transmembrane domain
betant: WO 0063373 A 12 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
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Lawson, A.D.G. and Finney, H.M.
Synthetic transmembrane components
Patent: JP 2002541845-A 12 10-DEC-2002;
CELITECH THERAPEUTICS LTD
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                                            94 bp
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                                                                                                                                                                                                                                            A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain Patent: WO 0063373.A 11 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB) LOCATION/QUALIFIERS
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Matches 53; Conservative 0; Mismatches 21;
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                               Sequence 11 from Patent W00063373.
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                                                                                                                       1 (bases 1 to 78)
Tsuji,S. and Sanpei,K.
Method for diagnosing spinocerebellar ataxia type 2 and primers
                                                                                                       1179 AGAGCGGGAGCGCCAGGAGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGA
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Sequence 12 from patent US 6251589.
AR159552
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Hyla chrysoscelis DNA for simple sequence repeat (SSR), isolate
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Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krenz,J.D., Semlitsch,R.D., Gerhardt,H.C. and Mahoney,P.A.
Isolation and characterization of simple sequence repeat loci in
the gray tree frog, Hyla chrysoscelis
Unpublished
                                                                                                                                                  1195 GAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGGAGCTG
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/rpt_unit="12. .13"
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Hyla chrysoscelis (southern gray treefrog)
Hyla chrysoscelis
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Score 38; DB 6; I
Pred. No. 1.4e+03;
0; Mismatches 25;
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April 28, 2005, 05:12:48; Search time 1763.82 Seconds (without alignments) 12223.299 Million cell updates/sec

US-09-674-237B-2 3642

score: Perfect

1 atggctcagtttcccacacc......tggaccccagccagcaatga 3642 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4530610 Total number of hits satisfying chosen parameters: 4390206 segs, 2959870667 residues Searched:

length: 0 length: 100 Bed sed Minimum.DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq_16Dec04:* geneseqn1980s:*geneseqn1990s:* Database

geneseqn2003as:*geneseqn2003bs:* geneseqn2002bs:* geneseqn2001bs: geneseqn2000s:* geneseqn2001as: geneseqn2002as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003ds:*

Abcose-Aac65406 Oligonuc-Aac65407 Oligonucl Ac634308 Human col Adc16446 Short înt Adc16445 Short int Aac65404 Oligonucl Aac65405 Oligonucl Abk89299 Trinucleo Adp49483 Oligonucl Abn38018 Human spl Human gen Oligonucl Aac65408 Oligonucl Aav17230 SCA2 gene Aai26445 Probe #16 SCA2 gene SCA2 gene 29 mer ol SCA2 gene Description Aav17232 Aav17233 Ads31430 Aac65409 Aad30431 Aac65405 Abk89299 SUMMARIES ADC16445 AAC65404 AAC65405 ABK89299 AAC65406 AAC65406 AAC65407 ADS31430 AAC65409 ADP49483 AAV17232 AAV17233 AAD30431 AAC65408 n 出 Query Match Length 0.00 42.8 42.8 41.8 40.4 40.4 39.2 36.6 36.4 35.8 33.4 Score 37.6 Regult No. υ

AAV17230 AAI26445

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Aba74544 Human foe Aai55023 Probe #23 Aba33360 Probe #17 Aak49188 Human bra Aba23711 Human bra Aba22756 Human gen Aat78908 Poly-glut Aav17234 SCA2 gene Adg5148 Synthetic Adg51429 Human gen Adg5148 Synthetic	Adcobole KRT19 PCR Adh58952 Silk prot Adh8415 Human gen Adv87572 Nucleotid Adq95147 Synthetic Abv88298 Human POS Adi84741 Human pol Adcobole Adv88298 Human gen Adv88107 Antifreez Adv88107 Antifreez Adv88107 Antifreez Adv88107 Antifreez Adv88105 Synthetic Adv88105 Synthetic
4 ABA74544 4 AA155023 AA155023 4 AA859360 4 AAK23011 4 AAK23011 4 ABS49832 6 AAT78908 2 AAT78908 13 AD095148 13 AD095148 4 AAC65410	13 AACCS411 13 ADMS00028 12 ADMS952 2 AAV27572 13 ADQ95147 6 ABV89298 AAC10510 12 AAC88107 2 AAC88107 2 AAC88106
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

orthologue; homology; expression distribution; Oligonucleotide array related rat oligonucleotide probe No 99. oligonucleotide array, orthologue, homo change, gene-expression, rat, probe, ss BP. 14-JUN-2002; 2002JP-00174208. 14-JUN-2002; 2002JP-00174208 ADP49483 standard; DNA; 80 (first entry) (HITA) HITACHI LTD Rattus norvegicus. JP2004016070-A. 22-JAN-2004. 12-AUG-2004 ADP49483; RESULT 1 ADP49483

WPI; 2004-113862/12

Oligonucleotide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonucleotides derived from ortholog gene of different organism immobilized on support.

Disclosure; Page 16; 56pp; Japanese.

The invention relates to a novel oligonucleotide array comprising a number of oligonucleotides derived from an orthologue gene of a different organism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different organisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the orthologue gene of the organism A and organism B. The sequence match degree of the organism species A and the organism species B is less than 70%. The sequence homology of the genes other than the orthologue gene of

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temperature of the variant genes other than the orthologue gene of temperature of the variant genes other than the orthologue gene of the organism species B is 20 degrees C or more. The oligonucleotide array is useful for measuring expression distribution of the orthologue gene in different organisms. The method is useful for comparing expression change of the orthologue gene with respect to medical-agent administration and for comparing change of the function of the orthologue gene in different organisms. The oligonucleotide array has the ability to perform a measurement of gene-expression distribution of two or more types of organism simultaneously. The oligonucleotide array improves reliability of measurement. This polynucleotide sequence represents a probe of a rat gene for comparison against a human gene used
the organism species A and the organism species B is the level-of-statistical-significance value, calculated using the homology searching algorithm: basic local alignment search tool (BLAST) and the value is 0.1 or more. The found value or the calculated value of the melting-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the oligonucleotide array of the invention.
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Sequence 80 BP; 19 A; 15 C; 25 G; 21 T; 0 U; 0 Other;

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2876
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                                              9
                               Gaps
                 ;;
 Length 80;
                0; Indels
2.2%; Score 80; DB 12; I
100.0%; Pred. No. 4.9e-09;
ive 0; Mismatches 0;
                                                               2877 GAAACTCATTTCAGGGCCCG 2896
                                                                       80; Conservative
         Local Similarity
                                                                              61
  Query Match
         Best Loca
Matches
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Human spliced transcript detection oligonucleotide SEQ ID NO:10766 Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss. ABN38018 standard; DNA; 60 BP (first entry) Homo sapiens 15-JUL-2002 ABN38018;

20-JUL-2001; 2001WO-IB001903. WO200210449-A2 07-FEB-2002.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-Shoshan A, Wasserman A, WPI; 2002-257383/30.

Faigler

Mintz L,

Mintz E,

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Example 1; SEQ ID NO 10766; 47pp; English.

specific genes.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several

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continuetorizes, each eagain of appearance of the genome, which encodes one or more messenger RNA splice variants. The which encodes one or more messenger RNA splice variants. The coligonoucleotide libraries are useful for detecting RNAs from a biological sample, in expression profilling studies, in qualitatively or biological sample, in expression profilling studies, in qualitatively or detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minical transcriptomes. The libraries may also be used as specialised minical interpretation of taste, and so allowing the detection of tissue coliogical or pathological state, and so allowing the detection of tissue coliogical or pathological state, and so allowing the detection of tissue coliogical or pathological state, and so allowing the detection of tissue specific genes such as those genes only expressed in specific genes; and to detect RNA transcriptom to detect colionate and splice containts of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from a particular containt invention. N.B. The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format containt of the printed specification, but was obtained in electronic format containts of the printed specification int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Short interfering double-stranded RNA oligonucleotide SEQ ID NO:171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds.
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oligonucleotides, each capable of hybridising selectively to messenger RNAs transcribed from a given transcription unit of
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Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60 BP; 19 A; 17 C; 13 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48.8; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.13;
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IMPERIAL COLLEGE INNOVATIONS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 71; SEQ ID NO 171; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3
Best Local Similarity 88.3
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-248169/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a target gene.
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ADC16446/c
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inhibition of expression of a target gene, where (I) comprises double stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang having a length of 0-inucleotide to 5-incleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (I); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNAs; (3) an array-based method of assessing a phenotypic effect of a double-stranded RNA on a target gene; (4) validating a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene comprising any of 311 20-78 cullibiting expression of a target gene comprising any of 311 20-78 cullibiting expression of a target gene comprising any of the sequence genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. cancer
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1187 AGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1246 Gaps ; 0 1.2%; Score 42.8; DB 10; Length 81; 71.8%; Pred. No. 3.9; ve 0; Mismatches 22; Indels (Sequence 81 BP; 0 A; 27 C; 27 G; 0 T; 27 U; 0 Other; 1247 GGGAGCTGGAGCGGCAGC 1264 20 AGCAGCAGCAGCAGC 3 Local Similarity 71.8%; 56; Conservative 88 Query Match Matches 셤 ò ઠે

21

ADC16445 standard; RNA; 81 BP ADC16445; RESULT 4 ADC16445 THE CONTRACT OF THE CONTRACT O

(first entry) 18-DEC-2003 Short interfering double-stranded RNA oligonucleotide SEQ ID NO:170.

expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds.

Synthetic

WO2003012052-A2.

13-FEB-2003

30-JUL-2002; 2002WO-US024226.

30-JUL-2001; 2001US-0308640P. 08-APR-2002; 2002US-0370970P.

(USSH) US DEPT HEALTH & HUMAN SERVICES. (CARN-) CARNEGIE INST WASHINGTON. (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S; Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;

WPI; 2003-248169/24.

New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression

Finney HM, Lawson ADG;

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The present invention describes an RNA (I) used for the interference or inhibition of expression of a target gene, where (I) comprises double stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang a length of 0-nucleotides in length and a 3' or 5' overhang contains a length of 0-nucleotide to 5-nucleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell or expression of a target gene in a cell or expression of a target gene in a cell or expression of a target gene in a cell or expression and sed responding array comprising a substantially flat substrante, and addressably arrayed different double-stranded RNAs; (3) an array-based method of assessing a comprising a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and condition of a target gene condition; and condition of a target gene condition are condition; and condition of a target gene condition; and condi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane-associated protein; antiviral; antibacterial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory; anticancer; antinflammatory; antiasthmatic;
antidiabetic; neuroprotective; chimeric receptor; infection;
inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eczema, cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 81 BP; 27 A; 27 C; 27 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 1.2%; Score 42.8; DE Local Similarity 71.8%; Pred. No. 3.9; See 56; Conservative 0; Mismatches
                                                    Claim 71; SEQ ID NO 170; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AGCAGCAGCAGCAGC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransmembrane domain; ss
  of a target gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200063373-A1.
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of membrane-associated

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The present sequence was used in the construction of chimeric receptors.

The properties and level of expression of a membrane-associated protein
may be altered by substituting a transmembrane region or a membrane-
anchoring region for transmembrane or membrane-anchoring regions that are
not naturally part of the protein. The relative response of membrane-
associated proteins to cell surface-associated antigen versus antigen in
solution, and the sensitivity of intracellular signaling mediated by
membrane-associated proteins can be altered. They can be important in
treatment of, e.g. HIV infection, bacterial infections, parasitic
infections, inflammatory/autoimmune disorders (e.g. relemantoid arthritis,
osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic
diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic
fibrosis or sickle cell anaemia), dermatological disorders (e.g.
psoriasis), neurological disorders (e.g. multiple sclerosis), organ
transplant rejection, graft-versus-host diseases, or metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chechechechechechedagenechechechechechechechechechechecheche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Membrane-associated protein; antiviral; antibacterial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory; disorder; autoimmune disorder; cancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes;
                               Altering the properties or level of expression of membrane-associate proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide B6464 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 98 BP; 2.A; 37 C; 25 G; 34 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1246 CGGGAGCTGGAGCGCCAGCGAGAGG 1270
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                                                                                                              Example 2; Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC65405 standard; DNA; 100 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2000; 2000WO-GB001471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finney HM, Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-015774/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 58; Conserva'
WPI; 2001-015774/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200063373-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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1186 GAGCGCCAGGAGCAGGACGACCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGGAGCAG 1245
                                                                                                                                                                                    anchoring region for transmembrane or membrane-anchoring regions that are anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic fibrosis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-
          Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; trinucleotide repeat instability; TNR; cancer; ds; fragile X syndrome; Huntington's disease; myoconic dystrophy; spinal and bulbar muscular atrophy; SBMA; SCA I; Kennedy's disease; spinocerebellar ataxia type I; Friedreich's ataxia; DRPLA; Gentatorubaral-palidoluyalan atrophy; SCA8; SCA12; SCA2; SCA6; SCA7; SCA3; Machado-Joseph disease; testicular cancer; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 100 BP; 34 A; 26 C; 38 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.8; DB Fred. No. 7.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1246 CGGGAGCTGGAGCGCCAGCGAGAGG 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCAGGAGCAGCACCCAAAAG 99
                                                                                               Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2001; 2001WO-US049800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2000; 2000US-00742025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 68.2%;
tes 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trinucleotide repeat CAG25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK89299 standard; DNA; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK89299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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; 0

27; Indels

0; Mismatches

Score 41.8; DB 4; Length 98; Pred. No. 7.4;

Detecting alterations in trinucleotide repeat (TNR) tract lengths in

Miret JJ;

Lahue RS, Pelletier R, (UYNE-) UNIV NEBRASKA

WPI; 2002-575460/61

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The invention relates to detecting (M1) alterations in trinucleotide repeat (TNR) tract lengths comprising: (i) contacting mammalian cells with a shuttle vector (containing approximately 25 repeats) that enters and replicates in the cells; (ii) introducing the vector into a yeast cell in the presence of a selection agent or (where the expanded TNR confers a His+ phenotype) in the absence of histidine, alteration to the TNR tract confers resistance to the selective agent or His+ phenotype; and (iv) selecting yeast cells with the shuttle vector containing TNR tract confers that survived the presence of the selective agent. Also included is an adaptation of the used to detect the contraction of 33 or 55 repeats using growth of the yeast cells in the absence of uracil. The methods of the present invention are useful for identifying disorders methods of the present invention are useful for identifying disorders (e.g. testicular and prostate), Fragile X Syndrome, Huntington's disease, myterious disease, myterious disease, myterious displaced and prostate, Pragile X Syndrome, Huntington's disease, myterious displaced and prostate), Fragile X Syndrome, Huntington's disease, myterious displaced and prostate of the macular atrophy (SMM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spinocerebellar ataxias (types 1, 8, 12, 3 (Machado- Joseph disease), 6, 7 and 2), dentatorubaral-palidoluysian atrophy (DRPLA); Fritedracich's ataxia and Kennedy's disease. The present sequence is the CAG25 TNR known to be unstable in Human sperm and in yeast which was tested in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian cells useful for identifying disorders associated with TNR instability such as cancer, Fragile X syndrome, Huntington's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane-associated protein, antiviral, antibacterial, antiparasitic, immunomodulatory, anticancer, antibirlammatory, anticathetic, antidiabetic, neuroprotective, chimeric receptor, infection, inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 6; Length 75;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eczema, cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide B6465 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 75 BP; 25 A; 25 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                          Example 1; Page 24; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be unstable in Human sperm a
the invention for expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC65406 standard; DNA; 92 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%;
Local Similarity 72.6%;
les 53; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2000; 2000WO-GB001471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1252 CTGGAGCGGCAGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAGCAGCAGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane domain; ss
                                               myotonic dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40200063373-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC65406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
  g
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(CLLT) CELLTECH THERAPEUTICS LTD

99GB-00008816.

16-APR-1999;

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1179 AGAGCGGGAGCGCCAGGAGCAGGAGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGA 1238
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                                                                                                                                                                                                                                                                                                 The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-anchoring region for transmembrane or membrane-anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, in the contraction of the contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rèjection, graft-versus-host diseases, or metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                   Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 agaacaggagcagcagcagcagcagagcaggagcagcaggagcaggagcaggagcaggagca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-associated protein, antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chineric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; eczema; oystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide B6466 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92 BP; 2 A; 34 C; 24 G; 32 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 71.6%; Pred. No. 16; les 53; Conservative 0; Minmart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                 Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC65407 standard; DNA; 94 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2000; 2000WO-GB001471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1239 GAAGCAGCGGGAGC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGAGCAGCAGC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases (e.g. diabetes)
   Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finney HM, Lawson ADG;
                                                         WPI; 2001-015774/02.
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   Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC65407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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WPI; 2003-182626/18.

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much reactions of successions of a membrane anothoring regions that are not naturally part of the protein. The relative response of membrane or naturally part of the protein. The relative response of membrane not naturally part of the protein. The relative response of membrane-sassociated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic proteins or sickle cell anaemia), dermatological disorders (e.g. cystic psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, gartt-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                   The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-
                                                                              Altering the properties or level of expression of membrane-associating proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94 BP; 32 A; 25 C; 35 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                Example 2; Fig 3; 47pp; English
                            WPI; 2001-015774/02
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1179 AGAGCGGGAGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGCAGCTGGA 1238
                                                           0; Gaps
DB 4; Length 94;
                     21; Indels
Score 40.4; DI
Pred. No. 16;
0; Mismatches
                                                                                         GAAGCAGCGGGAGC 1252
        .1 Similarity 71.6%;
53; Conservative
                                                                                                               84
                                                                                                             GCAGGAGCAGCAGC
Query Match
Best Local S:
Matches 53,
                                                                                         1239
                                                                                                               7
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Human colon cancer cell expressed cDNA #2720.
ACD94308 standard; cDNA; 97 BP.
            (first entry)
            23-SEP-2003
      ACD94308;
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breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolarance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; Open reading frame detection; genome sequencing; colon cancer; gene; ss.

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99US-00406117.
                                                                                                               98US-00196716.
                                                                                                                                          SIMPSON A J G.
                           US2002155438-A1.
Homo sapiens.
                                                                                  27-SEP-1999;
                                                                                                               20-NOV-1998;
                                                       24-OCT-2002.
                                                                                                                                          (SIMP/)
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Brentani RR;

Simpson AJG, Neto ED,

NETO E D. BRENTANI R'R.

(NETO/) (BREN/)

The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded coDNA by reverse transcribing mRNA with (I), amplifying single-stranded cDNA by reverse transcribing mRNA with (I), amplifying con amplifying steps with different primers and sequencing, preparing and properties and sequencing that a known manipulating sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleic acid molecule from a genome of an organism; and for sequencing all or part of agenome of an organism. mRNA is obtained from mammalian cor human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of large or small populations of subjects and can be used to carry out genetic analyses of populations of subjects and can be used to study living systems to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with diseases such as cancer, to determine antibiotic resistance or non-tolerance, and so forth. The method can also be used to offspring through ova or sperm. The analyses for pathological conditions can be crucial diseases, and the risk of affliction to a foetus, as well as through ova or sperm. The analyses for pathological conditions can be crucial out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of corps corps.

C carried out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be crucially to be passed to the genome can also be studied in this way. Similarly, the method erope crops retroviruses and other integrating viruses such as influenced as p 1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAAGCAGCTGGAGAAGCAGCAGCGGGAGAGCTGG 1255 trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of 0; Gaps nucleic acid analysis; variation assessment; neurological disease; Huntington's chorea; PCR suppression; ss. 1.1%; Score 39.2; DB 10; Length 97; 33.4%; Pred. No. 31; Ve 0; Mismatches 34; Indels 0 Clone #8 fragment identified by CAG repeat analysis method repeat; human; genome analysis; medical diagnostic; Sequence 97 BP; 0 A; 39 C; 0 G; 57 T; 0 U; 1 Other; 1256 AGCGCCAGCGAGAGGAGGAGGAGGAGGAGA 1288 AGAAGAAGAAGAAGAAGAAGAAGAAGA 4 Example 9; Page 407; 959pp; English AAV68382 standard; DNA; 89 BP. Local Similarity 63.4%; es 59; Conservative (first entry) Determining ope 10-MAR-1999 individual Query Match AAV68382; AAV68382/c Matches RESULT 11 à 셤 ò g

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1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCGGGAG 1251
                                                                                                                                                                                                                                                                                                                                                            This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                          Diagnosing spinocerebellar ataxis type II of CAG repeat units.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCA2 gene CAG repeat unit fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1252 CTGGAGCGGCAGCGAGAG 1269
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                                                                                                    96WO-JP001999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 67.9°
Matches 53; Conservative
                                                                                                                                                                                                                       WPI; 1998-120796/11
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                                                                                                                                                                                   Sanpei K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanpei K;
                                                                                                                                         (SRLS-) SRL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SRLS-) SRL INC.
                                                            18-JUL-1996;
                                                                                                    18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1996;
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                      29-JAN-1998
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                                                                                                                                                                                   Tsuji S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV17233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1183 CGGGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAG 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of a human CAG repeat containing clone DNA sequence isolated using the method of the invention. The method is for analysing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CAG repeat and a polymerase and PCR reagents; (b) preparing the nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid with the first and second primers; and (d) detecting the amplified product. The method is used to distinguish between the expression of genes in two or more blological samples, e.g. body fluids, cells, solid tissue or solid and liquid foods. It can be used in medical diagnostics, e.g. to differentiate between normal and diseased tissue or to assess the variation within monozygotic twin pairs. The method allows the isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorea. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types. Genome complexity is reduced by the new method which targets genomic subsets containing CAG repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysing nucleic acid samples - using amplification primers which contain CAG or CTG tri:nucleotide repeats for differential display of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 39; DB 2; Length 89; 65.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 89 BP; 2 A; 23 C; 37 G; 27 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCA2 gene CAG repeat unit fragment.
                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 32; 44pp; English
                                                                                                                                                                                                                                                                                                                                                            samples from different sources.
                                                                                                                                                          97US-0045078P
                                                                                                                    98WO-US008616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV17232 standard; DNA; 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Conservative
                                                                                                                                                                                                                                                                               WPI; 1998-594983/50.
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                                                                                                                                                                                                (UYBO-) UNIV BOSTON
Homo sapiens
                                     WO9849345-A1
                                                                                                                                                          29-APR-1997;
                                                                                                                    29-APR-1998;
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                                                                             05-NOV-1998
                                                                                                                                                                                                                                       Smith CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
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Diagnosing spinocerebellar ataxis type II - by PCR and determining number of CAG repeat units.

SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.

WO9803679-A1.

Synthetic

Matches

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Disclosure; Page 13-14; 23pp; Japanese.

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0; Gaps

DB 2; Length 78; 25; Indels

by PCR and determining number

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The invention relates to a nucleic acid hybridisation probe comprising a labelled, single copy nucleic acids of at least 50 nuclectides, which will hybridise to a deduced single copy sequence interval in traget nucleic acid (TNA) of known sequence. The single copy sequence is deduced by comparing the target nucleic acid (e.g. a disease causing gene) with a collection of high and low complexity repeat sequences as found in the genome of the organism from containing the target nucleic acid. The probe is generated by PCR on the target sequence. The probe is essentially free of blocking nucleic acid sequences which will hybridise to repeat equences within the genome of which the TNA is a part, and is labelled with a label selected from fluorochrome-responsive labels, fluorochromes, calorimetric chemical, conjugated proteins, antibodies, antigens and
                                                                                                                                                                                                                                                          1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCGGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single copy genomic hybridization probes for detecting specific nucleic acid sequences in sample by in situ hybridization useful for detection of acquired or inherited genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA; low complexity repeat; in situ hybridisation; Southern bloc; chromosome breakpoint; inherited genetic disease; neoplastic disorder; chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.
This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                          Score 38; DB 2; Length 78; Pred. No. 55;
                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome low complexity tandem repeat sequence #17.
                                                                                                                                         Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          1252 CTGGAGCGCCAGCGAGAG 1269
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                                                                                                                                                                                                 1 Similarity 67.9%;
53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS31430 standard; DNA; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knoll JHM, Rogan PK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-062378/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KNOL/) KNOLL J H M. (ROGA/) ROGAN P K.
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their mixtures. The probe is useful in a hybridisation method, where the hybridisation method is from in situ hybridisation, Southern blot, and cother methods in which nucleic acid is immobilised, where the method further comprises selecting a single copy nucleic acid which will confirm the comprises selecting a single copy nucleic acid which will confirm the comprises selecting a single copy nucleic acid which will confirm the probe in useful confirmation or triplicon sequence domain. The probe is useful for the genome. The genome at more than three preferably ten different locations as a determination of new repeat sequence family, where the determining step comprises selecting the single copy sequence from a duplicon or triplicon sequence domain. The probe is useful for chermining a chromosome breakpoint and is useful in the fields for determining a chromosome breakpoint and is useful in the fields for cycogenetics and molecular genetics for determining the presence of specific nucleic acid sequences in a sample of eukaryotic origin, e.g. the probes may be used to analyse specific chromosomal locations by in situ hybridisation as a detertion of acquired or inherited genetic diseases especially for detection of acquired or inherited genetic diseases especially for detection of genetic or neoplastic disorders. Unlike prior art techniques, the probe permits more precise chromosomal breakpoint determinations by in situ hybridisation defective, comprising the human HIRA gene (histone call corp lead to bigocyce and to comprising the human HIRA gene (histone call corp lead to bigocyce and intervals for use as probes of the invention. HIRA is located on chromosome 22 as a duplicate, deletions of locyp lead to bigocyce and chromosome 22 as a duplicate, deletions of locyp lead to bigocyce and chromosome region found within the human genome used to analyse the HIRA gene for repeat found within the human genome was organized to analyse the HIRA gene for the prepeat found within the human encome used to analyse the HIRA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the printed specification, but was obtained in electronic format directly from USPTO at sequata; uspto.gov/sequence.html?DocID=20030224356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1197 GCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane-associated protein, antiviral, antibacterial, antiparasitic, immunomodulatory, anticancer, antinflammatory, antiasthmatic, antidiabetic, neuroprotective, chimeric receptor, infection, inflammatory disorder, autoimmune disorder; cancer, allergy, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69 BP; 23 A; 23 C; 23 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 37.6; DB
72.1%; Pred. No. 65;
[ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC65409 standard; DNA; 88 BP.
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(CLLT ) CELLTECH THERAPEUTICS LTD
                                                                             WPI; 2001-015774/02
                                       Finney HM,
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Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.

Example 2; Fig 3; 47pp; English.

osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes) The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in membrane-associated proteins to a literacellular signaling mediated by membrane-associated proteins can be altered if they can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthitis,

Sequence 88 BP; 30 A; 24 C; 32 G; 2 T; 0 U; 0 Other;

1182 GCGGGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAAAAGCAGCTGGAGAA 1241 0; Gaps Query Match
1.0%; Score 37; DB 4; Length 88;
Best Local Similarity 67.5%; Pred. No. 1e+02;
Matches 52; Conservative 0; Mismatches 25; Indels

1242 GCAGCGGGAGCTGGAGC 1258 ð

g

2 GCGTCACCCAGAACAGCAGGAGCAGTAGCAGGAGCAGCAGCAGCAGCAGGAGCAGGA 61

Search completed: April 28, 2005, 08:43:21 Job time : 1764.82 secs

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33 0.9 84 9 32.4 0.9 98 6 32.2 0.9 91 1 3.2 0.9 60 91 1	31.8 0.9 87 9 CG572499 31.8 0.9 94 8 A276761	31.8 0.9 100 5 BQ234425 31.6 0.9 88 5 BQ80943 31.6 0.9 91 1 A1316382	35 31.6 0.9 100 7 CV295497 CV295497 ESFRB3874 31.4 0.9 100 7 D18610 D18610 MV3GS01671 37 31.2 0.9 88 2 BE662032 BE662032 bellelo.Y 38 31.2 0.9 95 5 BQ234381 BQ234381 hd44f06.9	31.2 0.9 96 5 BQ234483 31.2 0.9 97 1 AI947161 31.2 0.9 98 1 AV674805	31.2 0.9 100 5 BQ237998 31 0.9 79 4 BG39382	30.8 0.8 93 5 BQ234365 BQ234365 BQ234365	ALIGNMENTS	1 36	ITION	Beguence. SSION CC199586 LON CC199586.1 GI:30479626	S IN		<pre>1 (bases 1 to 94) BayGenomics.</pre>		Genomics Consortium (BayGenomics) ics.ucsf.edu	Sequence tag generated by 5' RACE of total RNA from gene trap ES	gene are available upon request from BayGenomics. Annotation	http://www.graponics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=		rce . 1	/Organism="ruts" indecines // / / / / / / / / / / / / / / / / /	/stran="129 ola" /db_rref="taxon:10090"	rem ce	/Clone lib="bayeenomin" /note="Vector: pGT1Lx;	Ouery Match 2.6%; Score 94; DB 8; Length 94; Best Local Similarity 100.0%; Pred. No. 4.8e-12; Matches 44, Conservative 0, Mismatches 0, Indels 0, Gans 0.			AACAGCACGACAAAACTATGAGTGACTTAA 721
ប	0	n in in in i	พี่พี่พี่พี่สั่		O	r 4 7		RESULT 1 CC199586	LOCUS	ACCESSION VERSION KENYMORDS	SOURCE	OKO	REFERENCE AUTHORS	TITLE JOURNI COMMENT				٠	on on the same	in the state of th				ORIGIN	Que		<u>ે</u> સ	a ò
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5.1.6 Compugen Ltd.		time 10842.9 Seconds ut alignments) 281 Million cell updates/sec	.tggaccccagccagcaatga 3642		S e	: 675282				• (<pre>cted by chance to have a of the result being printed, score distribution.</pre>			Description		X88324 H.Bapiens D	AZ786638 2M0032E18	AV533640 AV533640	AZ804535 ZM00651Z1 AZ471347 1M02851Z1	AZ837486 2M0132J14 AZ614077 1M0442B14		CK272899 Forward s CR256426 Reverse s AZ779622 2M0016114	CG565168 OST189766	CA3404/5 NISC_IZ04 CV030123 9138 Full	CO755195 Mdfrt3048 CCK459729 929944 MA
GenCore version 5.1.	search, using sw model	l 28, 2005, 06:48:09 ; Search tim (without a 12785.281	US-09-674-237B-2 3642 1 atggctcagttcccacacct	IDENTITY NUC Gapop 10.0 , Gapext 1.0	9544 segs, 19032134700 residues	satisfying chosen parameters	1: 0 1: 100	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	* · · · · · · · · · · · · · · · · · · ·	gb_estl:* gb_est2:* gb_htc:* gb_est3:*	JD	JD_EST6:* JD_GSS1:*		Le number of results prediction or equal to the score by analysis of the total	SUMMARIES		Length DB ID	94.	4.64.4	8 6 6	86 1	71 8	91 8	91 8	96 9 CR272899 0 89 9 CR256426 9 95 8 AZ779622	9,44,0	96 a	83 7 100 7
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GSS 29-MAY-1997

LOCUS DEFINITION

RESULT 2 AA589590

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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CC200157 46 bp mRNA linear GSS 09-MAY-2003
XG352 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 64)
Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome 21 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTCCCCAAGCAAGAACTATTCTTATGNAGTCAAGTTTACCACAGGCTCAGNTGGNTTCAA
  HSMC18D03 64 bp DNA linear GSS 29-M
H.sapiens DNA for trapped exon (ID HMC18D03), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, H.M., Rossier, C., Chrast, R. and Antonarakis, S.E. Cloning of trapped exons from human chromosome 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.6; DB 9; Length 64; Pred. No. 0.027;
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Genome Res. 6 (8), 747-760 (1996)
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    .64
/note="trapped exon"

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                                                                                                                                   Homo sapiens (human)
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                                                                                                                                   AA589590 179 bp mRNA linear EST 16-SEP-1997 A45099. A194009 all Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:975568 3' similar to SW.YFJ4 YEAST P43603 HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 79)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCCATGTACACATACGAGAGTTCTGATCAAGGAGATTTAAAGTTTCAGCAAGGAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conteact: Marram M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%; Score 74.2; DB 1; Length 79; 96.2%; Pred. No. 3.8e-07; Live 0; Mismatches 3; Indels
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Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 1.

Location/Qualifiers
AACAGCCACGACAAAACTATGAGTGGACACTTAA 94
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/clone="IMAGE:975568"
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/strain="C57BL/6"
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Matches 76; Conserv
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Fax: 801 585 7177
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2M0032E18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0032E18 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG352
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Mus musculus

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 92)

2 (bases 1 to 92)

3 (bases 1 to 92)

3 (bases 1 to 92)

4 (bases 1 to 92
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/note="Wector: PWD4Zlry; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTILxf"
/note="Vector: pGT1Lxf"
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 92.
                                                                                                                                                                                                        /organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="CS7BL/6J"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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                                                                                                  Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="129 ola"
information available from
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                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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Matches 46; Conservative
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Fax: 801 585 7177
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Genome Center
Winersity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
RM. 308, Blomedical Polymers Research
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1M0245A17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0245A17 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Insert Length: 10000 Std Exror: 0.00
Plate: 0245 row: A column: 17
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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/clone="UUGC1M0245A17"
/sex="Male"
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Location/Qualifiers
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Mus musculus
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AZ448190.1 GI:10600743
GSS.
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Similarity 69.6%;
55; Conservative
Best Local Similarity
Matches 55; Conserv
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                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gil 4732114|gbl=A72972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-tandant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
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Kazusa DNA Research Institute
Yana 1532-3, Kiaazau, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone lib="Arabidopsis thaliana flower buds Columbia"
/note="Vector: pBluescriptII SK-; Site_1: BcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/clone="FB065d08F"
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/ecotype="Columbia"
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AV533640/c
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셤 8 1.1%; Score 40.6; DB 1; Length 86;

Query Match

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi | 4732114 | gb | AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                                                              1200 GGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCG
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Junn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenn, E., Pedersen, T., Niederhausern, A. and Wright, D., Weises, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R., Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ804535
2M0065I21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic cone UUGC2M0065I21 R, genomic survey sequence.
                                                                                                                                                                      79 GGAGGAGAAGCAACGGGAGGAGGAGAAGCGACTGGAGGAGGAGGAGTAGCTGGTGGAGGA 20
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                                    0; Gaps
                                    24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
Pred. No. 87;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 0065 row: I column: 21
Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comparate: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0065121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 94.
Location/Qualifiers
                                                                                                                                                                                                                                               1260 GCAGCGAGAGGAGAGA 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ804535
AZ804535.1 GI:12956858
                                                                                                                                                                                                                                                                                                                    19 GAAGCAGGAGGAGAAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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AZ837486/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ471347 100 DNA linear GSS 04-OCT-2000 1M0285121R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0285121 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                  1199 AGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGC 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T. Keilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                       Gaps
                                                                                                                                   ö
                                                                              Length 94;
                                                                           1.1%; Score 40.4; DB 8; Length 9 65.6%; Pred. No. 1e+02; ive 0; Mismatches 31; Indels
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 70285 row: I column: 21
Seg primer: CACACAGGAAACAGGTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                            1259 GGCAGCGAGAGGAGGAGGAGGAGGAGA 1288
                                                                                                                                                                                                                                                                                                                                                 62 AGGAGGAAGAGGAGGAGGAGGAGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 71.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UUGC1M0285121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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                                                                        Query Match 1.1*
Best Local Similarity 65.6*
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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AZ471347/c
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KEYWORDS
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TITLE

SOURCE

FEATURES

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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                     1219 GAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGGAGGAGGAGGGGG 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases I to. A).

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Stokes, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R.
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2M0132J14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0132J14 R, genomic survey sequence.
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/clome_lib="Mouse lokb plasmid UUGCNH library."
/note="Vector: PWD42nry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.0%; Score 36.4; DB 8; Length 71;
Best Local Similarity 70.0%; Pred. No. 9.1e+02;
Matches 49; Conservative 0; Mismatches 21; Indels
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Length: 10000 Std Error: 0.00
0132 row: J column: 14
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Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0132J14"
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Location/Qualifiers
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Mus musculus
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Unpublished (2000)
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Fax: 801 585 7177
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb[AR129072.1], a coop-number of pMD42 (gi[4732114]gb[AR129072.1]), a coop-number of inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and ppurified. The sheared, adaptored mouse DNA was annealed to adaptored wector DNA, and transformed into chemically-competent B. coli X110-GGld (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ614077 91 bp DNA linear GSS 13-DEC-2000 1M0442B14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0442B14 R, genomic survey sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 91)
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/clone llb="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Unpublished (2000)
Contact: Robert B. Weiss
Contact: Other Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                   1.0%; Score 36.2; DB 8; Length 87; 68.5%; Pred. No. 1.1e+03; tive 0; Mismatches 23; Indels
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Insert Length: 10000 Std Error: 0
Plate: 0442 row: B column: 14
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 91.
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0442B14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1272 GGAGGGGGGAGG 1284
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Fax: 801 585 7177
Email: ddunn@genet
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|$plA129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2001)
Contact: Walbot V
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( bases 1 to 91)
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/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for
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Possible ligation site so sequence was trimmed. Post-ligation
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/mol_type="genomic_DNA"
/cullivax==mixed_background_W23/A188/B73"
/db_xref="tasno:4577"
/tissue_type="leaf"
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Tel: 650 723 2227
Fax: 650 725 8221
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Stanford University
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Plate: 1006126 row: 1
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/organism="Zea mays"
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/close libe 1006 - RescueMu Grid G" (note="Organ: leaf; Vector: RescueMu (engineered from fnote="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rambb.iastace.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with
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Unpublished (2001)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Fax: 650 728 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006126 row: I
Class: transposon-tagged.
Location/Qualifiers
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|cultivar="mixed background W23/A188/B73"
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   64.3%; Pred. No. 1.2e+03;
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1006126H07.xl.1006 - RescueMu Grid
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/dev_stage="adult"
/lab_host="DH108"
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/dw stage="adult"
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                              extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Class: transposon-tagged.
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/cultivar="mixed_background_W23/A188/B73"
/db_xref="taxon:4577"
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64.3%; Pred. No. 1.2e+03;
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Contact: Walbot V
Department of Biological Sciences
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      RescueMu.
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Fax: 650 725 8221
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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1176 GAAAGAGCGGGAGCCCAGGAGCA 1199

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1.0%; Score 36; DB 8; Length 91;

Query Match

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RESULT 15
CR272899/C
CR272899
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DOCUS
DEFINITION
CR272899
CR27289
CR272899
CR272899
CR27280
CR2728
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Db 35 AAGAGGAAGAGGAAGGAGGAAGAGG 6
Search completed: April 29, 2005, 02:01:58
Job time: 10843.9 secs

1267 GAGGAGGAGGAGGAAGGAGTCGAGAGG 1296

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Query Match
1.0%; Score 35.6; DB 9; Length 96;
Best Local Similarity 62.2%; Pred. No. 1.6e+03;
Matches 56; Conservative 0; Mismatches 34; Indels

0; Gaps

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Sequence 11, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 462, App
Sequence 4823, Ap
                                                                                  April 28, 2005, 07:02:07; Search time 544.672 Seconds (without alignments) 10941.112 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-573-080A-463
US-09-573-080A-463
US-09-043-303-11
US-09-043-303-11
US-09-043-303-13
US-09-573-080A-462
US-09-573-080A-462
US-09-573-080A-462
US-08-56-978B-24
US-08-56-978B-24
US-08-56-978B-24
US-08-56-978B-24
US-08-56-978B-24
US-08-13-999C-14585
US-07-812-421-26
US-07-812-421-26
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US-08-860-038-15
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US-09-281-481A-7
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                                                                                                                                                                                                                                                        1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Match
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ce 15, Appl ce 88, Appl ce 65, Appl ce 57, Appl ce 28, Appl ce 66, Appl ce 66, Appl ce 66, Appl ce 67, Appl ce 67, Appl ce 67, Appl ce 68, Appl ce 67, Appl ce 67, Appl		a Type 2 and	; Gaps 0;	AGCGGGAG 1251 AGCAGCAG 60		AND METHOD OF GENERATIN
Sequence		for Diagnosing Spinocerebellar Alaxia Therefor US/09/043,303 PS-18 17-18	 Jength 78; Indels 0; 	cagaagcagaaggccaagcggcagctggagctggagaagctgggggggg		80A GENOMIC HYBRIDIZATION PROBES AND METHOD '573,080A
US-09-580-923-15 US-08-182-175A-88 US-08-474-633A-65 US-08-82-771-65 PCT-US92-06412-88 US-08-17-15-28-23 US-08-17-15-15-23 US-08-477-5088-58 US-08-477-5088-58 US-08-478-0188-58 US-08-478-0188-58 US-08-478-41A-25 US-08-474-791A-58 US-08-174-633A-66 US-08-144-633A-66 US-08-144-633A-66 US-08-823-771-66 US-08-823-771-66 US-08-823-771-66	ALIGNMENTS	RESULT 1 US-09-043-303-12 Sequence 12, Application US/09043303 Patent No. 6251589 GENERAL INFORMATION: APPLICANT: TSUJ, Shoji APPLICANT: SANPEI, Kazujiro TITLE OF INVENTION: Method for Diagnosing Spin TITLE OF INVENTION: Primers Therefor FILE REFERENCE: 0760-02418 CURRENT APPLICATION NUMBER: US/09/043,303 CURRENT APPLICATION NUMBER: PCT/1996/01999 EARLIER APPLICATION NUMBER: PCT/1996/01999 EARLIER FILING DATE: 1996-07-18 NUMBER OF SEQ ID NOS: 17 SEQ ID NO 12 LENGTH: 78 TYPE: DAA TYPE: DAA TYPE: DAA TYPE: DAA TYPE: DAA TYPE: DAA	Score 38; DB Pred. No. 3.7; 0; Mismatches	CGGCAGCTGGAGCTGGA cagcagcagcagca	1269 78	09573080A COPY GENOMIC HYBR 15/09/573,080A 5-16 3.0
0.000000000000000000000000000000000000		SULT 1 Sequence 12, Application US/09043303 Sequence 12, Application US/09043303 Sequence 12, Application US/09043303 GENERAL INFORMATION: APPLICANT: TSUJI, Shoji APPLICANT: SANPEI, Kazujiro TITLE OF INVENTION: Method for Diagrittle OF INVENTION: MUMBER: US/09/0 CURRENT APPLICATION NUMBER: US/09/0 CURRENT APPLICATION NUMBER: US/09/0 CURRENT APPLICATION NUMBER: PSALIER FILING DATE: 1996-07-18 NUMBER OF SEQ ID NOS: 17 SOCTWARE: Patentin Ver. 2.0 LENGTH: 78 TYPE: DNA ORGANISM: Homo sapiens	1.0%; ilarity 67.9%; Conservative	aggaggccaag agcagcagcag	CTGGAGCGGCAGCGAGAG 	oul TTER SINGLE (07 TUMBER: U TUMBER: U 479 Version
22 28 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 8 2 2 2 2 8 3 2 3 3 3 3		12. Applic. 625189 NFORMATION TI SANFEI, TI SANFEI, TINVENTION INVENTION APPLICATION APPLICATION APPLICATION FILLING DATI APPLICATION APPLICATION APPLICATION APPLICATION THOMATION THOMAT	Sim 3;			ULT 2 09-573-080A-463 equence 463, Application attent No. 6828097 ENERAL INFORMATION: APPLICANT: ROGAN, PETER TITLE OF INVENTION: FILE REFERENCE: CURRENT PLILING DATE: CURRENT PLILING DATE: CURRENT PLILING DATE: SOFTWARE: PARENTH: 20 NOS: SOFTWARE: PARENTH: VETER LENGTH: 69
0000 0000		RESULT 1 US-09-043-303-12 Sequence 12, A Petent No. 625 GENERAL INFORM APPLICANT: SA TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF SEQ CURRENT APPLI SOFTWARE: PAL SOFTWARE: PAL SOFTWARE: PAL SEQ ID NO 12 LENGTH: 78 LENGTH: 78 LENGTH: 78 LENGTH: 78 LENGTH: 78 LENGTH: 78 LENGTH: 18 LENGTH: 18 CORGANISM: HO US-09-043-303-12	Query Match Best Local Matches 5	Qy 1192 Db 1	Qy 1252 Db 61	RESULT 2 US-09-573-080A-463 Sequence 463, Applicat Patent No. 6828097 APPLICANT: JOAN, KNC APPLICANT: ROGAN, PR TITLE OF INVENTION: FILE REFERENCE: 303 CURRENT APPLICATION CURRENT PILING DATE: NUMBER OF SEQ ID NOS: SOFTWARE: Patentin SEQ ID NO 463 LENGTH: 69
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Gaps

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1196 AGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCGGGAGCTGG 1255
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SEQ ID NO 13
LENGTH: 69
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
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                                               FRATURE: OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many entherial genomes. Length of core repeating element is vari OTHER INFORMATION: able and is often polymorphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: SANPET, Kazujiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; TITLE OF INVENTION: Primers Therefor
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT APPLICATION NUMBER: PCT/JP96/01999
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; RARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SCGTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 78
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APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
FILE REPERBNCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT PILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4.4;
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Best Local Similarity 72.11
Matches 49; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                GCAGCAGC 68
      TYPE: DNA ORGANISM: Artificial
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US-09-573-080A-463
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US-09-043-303-10
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US-09-043-303-11
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SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN
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                                                                                                           APPLICANT: TSUJI, Shoji
APPLICANT: TSUJI, Shoji
APPLICANT: TSUJI, Kazujiro
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REPERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT APPLICATION NUMBER: US/1996/01999
EARLIER APPLICATION NUMBER: PCT/UP96/01999
EARLIER PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
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WUWBER OF EGO ID NOS: 479
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-573-080A-462; Application US/09573080A; Sequence 462, Application US/09573080A; Patent No. 6828097; GENERAL INFORMATION: APPLICANT: NOGAN, FORDER; TITLE OF INVENTION: SINGLE COFY GENOMI; FILE REFERENCE: 30307
US-09-043-303-13; Sequence 13, Application US/09043303; Patent No. 6251589; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.9%;
Best Local Similarity 73.7%;
Matches 42; Conservative (
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                                                                                                       81 GCGGCCGCTGGAGCTGGAGCAGGAGCCGAGATCACCACGGGTGCTGGAGCAGGAAGGGAC 22
                                                                                                                                                                                                                                                                                     Sequence 4823, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6703491

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 20105

LENGTH: 89
                              Gaps
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61.7%; Pred. No. 2.2e+02;
tive 0; Mismatches 31; indels
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Pred. No. 2.2e+02;
0; Mismatches 31; Indels
                         23; Indels
    Pred. No. 1.2e+02;
0; Mismatches 23
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 66.7%;
Matches 46; Conservative
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1 Similarity 61.7%;
50; Conservative
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Matches 50; Conservative
                                                                                                                                              1278 GAGGAAGGA 1286
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Best Local Similarity
Matches 50; Conserva
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US-09-270-767-20105/c
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1708 GCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCACCTCCGGGAGCAGCTGGAGGT 1763
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RESULT 9
US-08-556-978B-24
Sequence 24, Application US/08556978B
Sequence 24, Application US/08556978B
Sequence 24, Application US/08556978B
SEQUENCE OF INFORMATION
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
SEQUENCES: 107
CORRESPONDENCE ADDRESS:
STREET: 1007 MARKET STREET
CITY: WILMINTON
STREET: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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Pred. No. 4.1e+02;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-A
TELECOMMUNICATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1007 MARKET STREET
COUTY: WILMINTON
STATE: DELAMARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOAD, LINDA AXAMENTY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
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; Sequence 25, Application US/08556978B
; Patent No. 6268169
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Best Local Similarity 71.4%;
Matches 40; Conservative
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STRANDEDNESS: single
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1213 CAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAG 1263
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                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
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Patent No. 5925540
GENERAL INFORMATION:
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Best Local Similarity 59.3%;
Matches 48; Conservative
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US-09-513-999C-14585
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SOFTWARE: Patent.pm
SEQ ID NO 14585
LENGTH: 86
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OTHER INFORMATION: n=a,
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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US-09-513-999C-14585
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                                                                  US-08-068-747-1
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APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 93;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
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0.8%; Score 30.4; DB 3;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 40; Conservative 0; Mismatches 16;
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REPERENCE/DOCKET NUMBER: 369-A
TELECHONE: 302-892-8112
TELEPHONE: 302-773-0164
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
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US-08-068-747-1/c
Sequence 1, Application US/08068747
Patent No. 5695933
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 93 base pairs TYPE: nucleic acid stranbedness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-25
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SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Lexington
STATE: Massachusett
COUNTRY: USA
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1207 AAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAAGCAGCGGGAGCTGGAGCGGCAGCGA 1266
Sequence 14585, Application US/09513999C

Sequence 14585, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICANTION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
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APPLICANT: Thomas E.
APPLICANT: Thomas E.
APPLICANT: Szumanski, Maria B.W.
ITILE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: 43
CORRESPONDENCE ADDRESS: WHITHAM, CHRIIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 4; Length 86;
Pred. No. 5e+02;
1; Mismatches 32; Indels
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Gaps

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1210 CGGCAGCTGGAGGCTGGAAAGCAGCTGGAGAAGCAGCGGGAAGCTGGAGCGGCAGCAGC 1264
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GENERAL INCRMATION:
APPLICANT: Toth, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
ATILE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

CLASSIFICATION TO 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION TO 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELEFORMICATION INFORMATION:

TELEFORMICATION INFORMATION:

TELEFORMICATION NUMBER:

TELEFORMICATION TO 391.2510
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/07814220 Patent No. 5925540
                     REGISTATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.
TELECOMMUNICATION INFORMATION:
TELEFRAX: 703-391-2510
TELEFRAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.9
Matches 39, Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                            linear
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; Patent No. 5932697
; GENERAL INFORMATION:
APPLICANT: Caccei, Thomas E.
APPLICANT: Toth, Thomas E.
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ITILE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CTOW. Destro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.8%; Score 29.4; DB 2; Length 57; Best Local Similarity 70.9%; Pred. No. 5.6e+02; Matches 39; Conservative 0; Mismatches 16; Indels
                                                                                             COMPUTER: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC Compatible
CORRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REGISTRATION NUMBER: 32,635
REGISTRATION NUMBER: 01.016
TELEFHONE: 703-391-2510
TELEFNOWE: 703-391-2510
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ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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/desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: 1i.
; MOLECULE TYPE:
; DESCRIPTION:
US-07-814-220-26
                                                                             20191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-812-421-26
                                                    COUNTRY:
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0; Gaps Query Match 0.8%; Score 29.4; DB 2; Length 62; Best Local Similarity 70.9%; Pred. No. 5.9e+02; Matches 39; Conservative 0; Mismatches 16; Indels

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à g

Search completed: April 29, 2005, 02:23:45 Job time : 544.672 secs

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Query Match
Best Local Similarity
Matches 53; Conserv
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Sequence 463, App
Sequence 6, Appli
Sequence 8, Appli
                                                                                                                                                                April 28, 2005, 07:33:31 ; Search time 1939.12 Seconds (without alignments) 11433.739 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24680, A
Sequence 156, App
Sequence 462, App
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'cgnz_6/ptodata/1/puppna/bcryus/progens.seq:*
'cgnz_6/ptodata/1/puppna/USOB_NEW_PUB.seq:*
'cgnz_6/ptodata/1/puppna/USOB_NEW_PUB.seq:*
'cgnz_6/ptodata/1/puppna/USOB_PUBCOMB.seq:*
'cgnz_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
'cgnz_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
'cgnz_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
'cgnz_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
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'cgnz_6/ptodata/1/pubpna/USIOB_WWW_PUB.seq:*
'cgnz_6/ptodata/1/pubpna/USIOB_WWW_PUB.seq:*
'cgnz_6/ptodata/1/pubpna/USIOB_WWW_PUB.seq:*
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ptodata/1/pubpna/US06 PUBCOMB.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ptodata/1/pubpna/US07_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-786-9708-463

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US-10-313-8948-6

US-10-313-8948-6

US-10-313-8948-6

US-10-30-88-71-24680

US-10-759-7318-156

US-10-758-307-462

US-10-758-307-66

US-10-758-307-66
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/cgn2_6/ptodata/1/pubpna/PIT_NEI
/cgn2_6/ptodata/1/pubpna/PIT_NEI
/cgn2_6/ptodata/1/pubpna/USO6_PI
/cgn2_6/ptodata/1/pubpna/USO6_PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5642217 seqs, 3043843248 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY NUC
Gapop 10:0 , Gapext 1.0
                                                                                                                                                                                                                                                                                   US-09-674-237B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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1112 112 113 113 113 113 113 113 113 113	Sequence 55, Appl Sequence 58, Appl Sequence 3143, Appl Sequence 66, Appl Sequence 66, Appl Sequence 11, Appl Sequence 11, Appl Sequence 66, Appl Sequence 66, Appl Sequence 22933, A Sequence 22933, A Sequence 22933, A Sequence 22933, Sequence 22933, A
S-10-085-906-1 S-10-029-386-1 S-10-059-3186-1 S-10-061-201-1 S-10-059-3186-2 S-09-9189-687-2 S-09-9173-688-2 S-10-059-731A-2 S-10-051-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1 S-10-021-323-1	US-10-804-678-65 US-10-096-986-58 US-10-645-471A-31 US-10-645-471A-31 US-10-023-06A-66 US-10-023-06A-66 US-10-072-809A-11 US-10-071-323-808 US-09-38-97-14 US-10-333-678-66 US-09-964-761-2293 US-09-922-261-229 US-10-296-734-1351 US-10-296-734-1351
4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
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0 0 0 0 000000	00 00 0 0

ALIGNMENTS

APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: FAIGHER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE 1
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME Length 60; 1.3%; Score 48.8; DB 10; 88.3%; Pred. No. 0.0022; iive 0; Mismatches 7; TILE REPERENCE: 3668-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/281,724
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0 US-09-908-975-10766
Sequence 10766, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION: TYPE: DNA CRGANISM: Homo sapiens US-09-908-975-10766

1 GGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAAATCACTATCCAGGCCAGGACA 60

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Gaps .; 0

Indels

53; Conservative

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Sequence 66, P Sequence 339,

Sequence

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1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1251
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Sequence 8, Application US/10407818

Fublication No. US20040198971A1

GENERAL INFORMATION:
APPLICANT: RABANI, ELAZAR
APPLICANT: STRVRIANOPOLIOS, JANNIS G.
APPLICANT: DONEGAN, JAMES J.
TITLE OF INVENTION: MULTISIGNAL LABELING REAGENTS, AND PROCESSES AND USES
FILE REFERENCE: ENZ-65
CURRENT APPLICATION NUMBER: US/10/407,818
CURRENT PILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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1.0%; Score 34.6; DB 18; Length 63;
Best Local Similarity 75.4%; Pred. No. 27;
Matches 43; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:/note OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                          APPLICANT: Heing, Ann
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
FILE REPERENCE: 21108.0001U1
CURRENT PELLING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 36.6; DB 18;
Best Local Similarity 65.1%; Pred. No. 8.5;
Matches 54; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1252 CTGGAGCGCAGCGAGAGGAGGA 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 cagcaacagcagcaacagca 86
                                                                                                                         Sequence 6, Application US/10333894A Publication No. US20040259085A1 GENERAL INFORMATION: APPLICANT: Chang, Chawnshang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: 3'-amidated US-10-407-818-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
61 GCAGCAGC 68
                                                                                RESULT 4
US-10-333-894A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-333-894A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Sequence 463, Application US/10786970A
Sequence 463, Application US/10786970A
Sequence 463, Application No. US2005064449A1
SEMERAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: GOGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING FILE REFERENCE: 30307-704-02-24
PRIOR APPLICATION NUMBER: US/09/573,080
PRIOR PELLING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SEQ ID NO 463
LENGTH: 69
                                                                                                                                                    APPLICANT: JOAN, KNOLL H
APPLICANT: JOAN, KNOLL H
APPLICANT: GOAN, ENGEN GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in properties informany eucherial genomes. Length of core repeating element is vari; OTHER INFORMATION: able and is often polymorphi
US-10-786-97084-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari OTHER INFORMATION: able and is often polymorphic
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Best Local Similarity 72.1%; Pred. No. 3.9;
Matches 49; Conservative 0; Mismatches 19; Indels
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                                                                                                Sequence 463, Application US/09854867
Publication No. US20030224356A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 72.1%;
Matches 49; Conservative
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US-10-786-970A-463
                                                                                JS-09-854-867-463
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1210 CGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGGAGA 1268
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                                        Query Match
0.9%; Score 33.4; DB 9; Length 93;
Best Local Similarity 72.9%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 16; Indels
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Sequence 156, Application US/10759731A
Publication No. US20050079574A1
GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
FILE REFERENCE: 11669.1364911
CURRENT APPLICATION NUMBER: US/10/759,731A
CURRENT PILING DATE: 2004-01-16
PRIOR PELICATION NUMBER: US 60/441,059
PRIOR FILING DATE: 2003-01-16
PRIOR PLILING DATE: 2003-01-18
PRIOR PLILING DATE: 2003-01-18
PRIOR PLILING DATE: 2003-01-18
PRIOR PLILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn version 3.3
: SEQ ID NO 156
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NAME/KEY: misc_feature
LOCATION: (26)...(26)
OTHER INFORMATION: y is c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28)...(28)
OTHER INFORMATION: s is g or c
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LOCATION: (29)...(29)
OTHER INFORMATION: y is c or t
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LOCATION: (37)...(38)
OTHER INFORMATION: s is g or c
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LOCATION: (43)...(43)
OTHER INFORMATION: k is g or t
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ORGANISM: Artificial Sequence
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NAME/KEY: misc feature
LOCATION: (41)...(41)
OTHER INFORMATION: 8 is 9 or
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OTHER INFORMATION: m is
FEATURE:
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LOCATION: (34)..(35)
OTHER INFORMATION: s is
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OTHER INFORMATION: r is
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NAME/KEY: misc feature
LOCATION: (46)..(46)
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APPLICANT: PERU, SHARTON G.
APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HAUZE', DAVIG K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HAUZE', DAVIG K.
APPLICANT: CHEN, WENSHENGEN G. ACID FROBES USEFUL FOR ITILE OF INVENTION: GENE EXPENSION ANALYSIS BY MICROREAY CHEN G.
ITILE OF INVENTION: GENE EXPERSION ANALYSIS BY MICROREAY G.
CURRENT APPLICATION NUMBER: US OF 06/180, 312
PRIOR PELICATION NUMBER: US OF 06/180, 312
PRIOR PELICATION NUMBER: US OF 06/20, 456
PRIOR PELICATION NUMBER: OF 06/20, 456
PRIOR PELICATION NUMBER: PC 10/20, 10/20
PRIOR PELICATION NUMBER: PC 10/20, 40/20
PRIOR PELICATION NUMBER: PC 10/20, 40/20
PRIOR PLICATION NUMBER: PC 10/20, 40/20

N: EXPRESSED IN LUNG, SIGNAL = 2.8

N: EXPRESSED IN PLACENTA, SIGNAL = 1.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

N: EXPRESSED IN HELA, SIGNAL = 3.5

N: EXPRESSED IN HELA, SIGNAL = 3.9

N: EXPRESSED IN HEARIN, SIGNAL = 4.5

N: EXPRESSED IN HEART, SIGNAL = 4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6

N: N: THIT: q15031896, EVALUE 2.000-13

N: EST_HUMAN HIT: R18580.1, EVALUE 3.000-13
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SOFTWARE: Annomax Sequence Listing Engine vers, 1.1
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; Patent No. US20020048763A1
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 93
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Sequence 462, Application US/10786970A
Publication No. US20050064449A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOAN, RWOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
CURRENT APPLICATION NUMBER: US/10/786,970A
CURRENT FILING DATE: 2004-02-24
PRIOR PAPLICATION NUMBER: US/09/573,080
PRIOR PELING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SEQ ID NO 462
LENGTH: 69
                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphic US-09-854-867-462
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66.7%; Pred. No. 1.4e+02;
tive 0; Mismatches 23; Indels
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Publication No. US20040209290A1
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH, INC.
APPLICANT: RUSH UNIVERSITY MEDICAL CENTER
APPLICANT: Cobleigh, Melody
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SEQ TWARE: PatentIn version 3.1
SEQ ID NO 462
LENGTH: 69
                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                    TYPE: DNA
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Publication No. US20030224356Al
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL H
APPLICANT: ROGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAAAGCAGCGGGAGCTGG 1255
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; OTHER INFORMATION: k is g or t
US-10-759-731A-156
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LOCATION: (56)..(56)
OTHER INFORMATION: y is c or
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THER INFORMATION: y is c or
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THER INFORMATION: y is c or
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THER INFORMATION: 8 18 9 or
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OTHER INFORMATION: m is a or
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THER INFORMATION: Y IS
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THER INFORMATION: 8 is
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LOCATION: (58)...(58)
THER INFORMATION: k is
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THER INFORMATION: r is
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THER INFORMATION: 8 is
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LOCATION: (73)...(73)
                                             NAME/KEY: misc feature OCATION: (50)...(50)
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COCATION: (53)..(53)
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Best Local Similarity
Matches 36; Conserva
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US-09-854-867-462
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1186 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCAGAAAGCAGCTGGAGAAGCAG 1245
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| Sequence 339, Application US/10852797
| Publication No. US20050064455A1
| GENERAL INFORMATION:
| APPLICANT: Genomic Health, Inc.
| APPLICANT: Baker, Joffre
| APPLICANT: Baker, Joffre
| APPLICANT: Shak, Steven
| APPLICANT: Shak, Steven
| APPLICANT: Soule, Sharon
| TITLE OF INVENTION: Response to Chemotherapy
| TITLE OF INVENTION UNMBER: 004/0010
| CURRENT FILING DATE: 2004-05-24
| PRIOR FILING DATE: 2003-05-28
| NUMBER OF SEQ ID NOS: 372
| SOFTWARE: FREUENCE: RestSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.2; DB 19; Length 77; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.2; DB 18; Length 77;
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APPLICANT: Cronin, Maureen
TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
TITLE OF INVENTION: CANCER PROGNOSIS
FILE REFERENCE: 39740/0008 US
CURRENT APPLICATION NUMBER: US/10/758,307
CURRENT APPLICATION NUMBER: US 60/440,861
PRIOR APPLICATION NUMBER: US 60/440,861
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 440
SOFTWARE PARISE PARISEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8e+02;
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Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 42; Conservative
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-085-906-174/c
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US-10-852-797-339
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LENGTH: 77
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Sequence 17340, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
GIRERAL APPLICANT: APPLICANTION: WINDER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARENT FILING DATE: Sequence Listing Engine vers. 1.1
SEQ ID NO 17340
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1169 AGGAGAGGAAAGAGCGGGAGCGCCAGGAGCAGGCGAAGCGGCAGCTGGAGCTGGAGA 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTINULATORY RECEPTOR LOCUS AND USES THEREOF
TITLE REPERENCE: GNN-5343CP2.
CURRENT PRILIG DATE: 2002-02-27
CURRENT FILING DATE: 1099-03-25
PRIOR PELING DATE: 1999-03-25
PRIOR PILING DATE: 1999-03-25
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 174
LENGTH: 86
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Pred. No. 4.2e+02;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.7 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8 OTHER INFORMATION: NT HIT: D86240.2, EVALUE 4.90e+00 US-10-029-386-17340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3e+02;
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 31.2;
60.7%; Pred. No. 3e-
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Best Local Similarity 63.5%;
Matches 47; Conservative
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Matches 51; Conservative
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CORGANISM: Homo sapiens
US-10-085-906-174
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RESULT 14
US-10-759-731A-155/C

Sequence 155, Application US/10759731A

Publication No. US20050079574A1

GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
FILE REFRENCE: 11669.136USU

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 60/441,059

PRIOR APPLICATION NUMBER: US 60/411,059

PRIOR PRILNG DATE: 2003-01-16

PRIOR PELING DATE: 2003-01-16

PRIOR PELING DATE: 2003-01-16

PRIOR FILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-0-18

SPRIOR FILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 194

SEQ ID NO 155

LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: RIG ala scan
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NAME/KRY: misc_feature
LOCATION: (34)...(35)
OTHER INFORMATION: s is g or c
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OTHER INFORMATION: m is a or c
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LOCATION: (49)...(49)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
NCATION: (32)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (41)...(41)

THER INFORMATION: Y is c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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LOCATION: (43) ... (43)
OTHER INFORMATION: k is g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (25)...(26)
OTHER INFORMATION: s is g or
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NAME/KEY: misc feature
LOCATION: (37)...(37)
OTHER INFORMATION: k is g (
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NAME/KEY: misc_feature
LOCATION: (44)...(44)
OTHER INFORMATION: y is c
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OTHER INFORMATION: y is c
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LOCATION: (28)...(28)
OTHER INFORMATION: r is
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OTHER INFORMATION: r is
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"^~~TOWN: (47)...(47)
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LOCATION: (29)..(29)
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NAME/KEY: misc_feature
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1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1255
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Publication No. US2030166229A1
GENERAL INFORMATION:
APPLICANT: Shamon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REPERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                     NAME/KEY: misc feature
LOCATION: (52)...(53)
OTHER INFORMATION: s is g or c
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NAME/KRX: misc feature
LOCATION: (65)-.(65)
OTHER INFORMATION: s is g or c
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                           LOCATION: (50)...(50)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                    LOCATION: (55)..(56)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (61)..(61)
OTHER INFORMATION: k is g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (68)...(68)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (70)...(70)
OTHER INFORMATION: r is a or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (64)...(64)
OTHER INFORMATION: k is g or t
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LOCATION: (73)...(73)
OTHER INFORMATION: k is g
                                                                                                                                                                                                                                                                                     LOCATION: (59)...(59)
OTHER INFORMATION: m is a
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc feature
LOCATION: (74)...(74)
NAME/KEY: misc_feature
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US-10-061-201-11
                                                                                                                                                                                               LOCATION:
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3514 GGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAGAAGTCAGT 3573

Gaps

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Score 30.4; DB 16; Length 96; Pred. No. 5.4e+02; 0; Mismatches 41; Indels

Query Match 0.8%; Best Local Similarity 57.3%; Matches 55; Conservative (

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Search completed: April 29, 2005, 03:41:19 Job time : 1940.12 secs

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Sequence:

Searched:

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PAT 30-JAN-2004
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AY23393 Arabidops
AX421455 Sequence
AX92149 Sequence
BD117008 EST and e
AX107476 Sequence
CQ542573 Sequence
CQ538403 Sequence
CQ725585 Sequence
AY045524 Panthera
AY184049 Drosophil
        AY184035 Drosophil
AY184060 Drosophil
AY184026 Drosophil
AY184026 Drosophil
AY545901 Fennerope
Y17097 Cladoberryu
AY545901 Fennerope
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AY293992 Arabidops
A43830 Sequence 4
II7407 Sequence 4
BD270475 Synthetic
AX039308 Sequence
AX039517 Sequence
                                                                         AY293995 Arabidops
AY29394 Arabidops
AY29394 Arabidops
AX530502 Sequence
AY184047 Drosophil
AY184053 Drosophil
AY184051 Drosophil
AY132812 Femerope
AX902306 Sequence
BD037839 Sequence
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                                                                                    Arabidops
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 10766 07-FEB-2002;
Ditylum
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Matches:
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/organism="Homo sapiens"
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AY184038
AY184047
AY184053
AY132812
AX902306
BD037839
         AY184035
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AY545903
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Location/Qualifiers
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AR208350 Sequence
AR208351 Sequence
AY545898 Fennerope
                                                                          (without alignments)
4849.920 Million cell updates/sec
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                                                                                                                         MAQPPTPFGGSLDVWAITVE.....VGLFPSNYVKLTTDMDPSQQ 1213
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                                                                April 28, 2005, 21:36:20 ; Search time 12119 Seconds
                                                                                                                                                                                                                           2238514
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                      4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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, Fgapext
, Delext
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Maximum DB seq length: 100
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Result No.

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Dawkins, R.Letts. and Abraham, L.Joseph:
Method for determining ancestral haplotypes using haplospecific geometric elements within the major histocompatibility complex multigene cluster

Patent: US 6383747-A 6 07-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 96)
Dawkins, R.Lettes. and Abraham, L. Joseph.
Method for determining ancestral haplotypes using haplospecific geometric elements within the major histocompatibility complex multigene cluster
Patent: US 633747-A 7 07-MAY-2002;
Location/Qualifiers
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                                                                            745 AlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIleGlnProGlyAsp
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/mol_type="unassigned DNA"
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CAGAGAGAGAGAGAGAGAGAGAGAGA 3
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98 bp DNA linear INV 08-MAR-2004
Fenneropenaeus chinensis clone TE1-122696 microsatellite sequence.
AY545898
AY545898.1 GI:44894761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z (bases 1 to 98)

Kong, J., Meng, X., Liu, P. and Gao, H.

Direct Submission

Submitted (07-FEB-2004) Germplasm Resources and Genetic Breeding
Laboratory, Yellow Sea Fisheries Research Institute, 106 Nanjing
Road, Qingdao, Shandong 266071, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GAGAGAGAGAGAGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penaeidae, Fenneropenaeus.

(bases 1 to 98)

Kong, J., Meng, K., Liu, P. and Gao, H.
Selection of polymorphic microsatellites from random shearing in Unpublished
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/note="microsatellite"
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Fenneropenaeus chinensis
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AF263002
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Location/Qualifiers
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                                                                                                                      Rynearson, T. A. and Armbrust, E. V.

Rynearson, T. A. and Armbrust, E. V.

DNA fingerprinting reveals extensive genetic diversity in a field by a fingerprinting reveals extensive genetic diversity in a field by a construct diatom Ditylum brightwellii

Limnol. Oceanogr. 45 (6), 1329-1340 (2000)

2 (Bases 1 to 91)

2 (Bases 1 to 91)

Direct Submission

Submitted (03-MAY-2000) Oceanography, University of Washington, Box 357940, Seattle, WA 98195, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY184035 99 bp DNA linear INV 27-FEB-2003
Drosophila melanogaster clone TTCTC28 centromeric satellite
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                                                                                                                                                                                                                                                                                                                                         /organism="Ditylum brightwellii"
/mol_type="genomic DNA"
/isolation_source="Ditylum brightwellii, clone CCMP 358;
Center for the Culture of Marine Phytoplankton"
/db xref="texon:49249"
/clone="Dbr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-NOV-2002) MCBL, The Salk Institute, 10010 N. Torrey Pines Rd., La Jolla, CA 92037, USA
                                                                                        Bacillariophyta; Coscinodiscophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neopera, Endoptery, Diptera, Brachycera, Muscomorpha, Beptydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 99)
Sun, X., Le, H.D., Wahlstrom, J.M. and Karpen, G.H.
Sun, X., e, H.D., Wahlstrom, J.M. and Karpen, G.H.
Sequence analysis of a functional Drosophila centromere Genome Res. 13 (2), 182-194 (2003)
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                                                                                        Bukaryota; stramenopiles;
Lithodesmiaceae; Ditylum.
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AY184035.1 GI:28193785
                      GI:9802316
                                                       Ditylum brightwellii
Ditylum brightwellii
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AY184060 99 bp DNA linear INV 27-FEB-2003
Drosophila melanogaster clone TTCTC53 centromeric satellite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases I to 99)
Sun.X., Le, H.D., Wahlstrom, J.M. and Karpen, G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
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Sun, X., Le, H.D., Wahlstrom, J.M. and Karpen, G.H.
Direct Submission
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   melanogaster"
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota,
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 100)
Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
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Drosophila melanogaster clone TTCTC19 centromeric satellite
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Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Direct Submission
Submitted (20.NOV-2002) MCBL, The Salk Institute, 10010 N. Torrey
Pines Rd., La Jolla, CA 92037, USA
                                                                      Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Sun, X., Le, H.D.; Wahlstrom, J.M. and Karpen, G.H.

Sequence analysis of a functional Drosophila centromere

Genome Res. 13 (2), 182-194 (2003)
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/map="centromere"
/clone="TTCTC19"
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Matches:
Conservative:
Mismatches:
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1. .99
/note="satellite"
                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
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/rpt_unit="ttctc"
                                                                                                                                                                                                                                                                                                     AY184026.1 GI:28193776
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74.50
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AY545903/c
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repeat_region
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Genetic and morphological characterization of Cladobotryum species
causing cobweb disease of mushrooms
Appl. Environ. Microbiol. 65 (2), 606-610 (1999)
99124595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 GlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArgArgGlu 434
                                                                                                                                                                   Kong, J., Meng, X., Liu, P. and Gao, H.
Selection of polymorphic microsatellites from random shearing DNA
clones in Fenneropenaeus chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                  Fenneropenaeus chinensis
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Fenneropenaeus.
1 (bases 1 to 90)
Fenneropenaeus chinensis clone TE4-43565 microsatellite sequence.
AY545903
                                                                                                                                                                                                                                                                                   Submitted (07-FEB-2004) Germplasm Resources and Genetic Breeding Laboratory, Yellow Sea Fisheries Research Institute, 106 Nanjing Road, Qingdao, Shandong 266071, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-APR-1998) G.J. McKay, Queens University Belfast, Department of Applied Plant Science, Newforge Lane, Belfast, N. Ireland BT9 5PX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Fenneropenaeus chinensis"
/mol_type="genomic DNA"
/db_xref="taxon:139456"
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Mismatches:
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Matches:
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Direct Submission
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/note="microsatellite"
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                                    AY545903.1 GI:44894766
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Hypomyces odoratus
Hypomyces odoratus
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AY545901 98 bp DNA linear INV 08-MAR-2004
Fenneropenaeus chinensis clone TE4-32234 microsatellite sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Penneropenaeus chinensis
Fenneropenaeus chinensis
Eukaryota; Metazoa; Athropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kong, J., Meng, X., Liu, P. and Gao, H. Selection of polymorphic microsatellites from random shearing DNA clones in Fenneropenaeus chinensis
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/mol_type="genomic DNA"
/db_xref="taxon:139456"
                                                                                                                                                                                                                                       93
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113
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Matches:
Conservative:
Mismatches:
Indels:
                                /organism="Hypomyces odoratus"
/mol type="genomic DNA"
/isolate="Z15001"
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                                                                                      /specific_host="Agaricus
/db_xref="taxon:76883"
                                                                                                                                                                                                                                       Length:
                                                                                                                          /tissue_type="mycelium"

    .98
    /note="microsatellite"

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Location/Qualifiers
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1 (bases 1 to 98)
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AY545901.1 GI:44894764
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72.00
75.00%
46.43%
1.15%
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76.92%
50.00%
1.16%
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8.1e+04
70.50
53.85%
43.59%
1.12%
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                             Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
               422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 LeuGluLeuGluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGlu 425
                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysargGlnLeuGluLeuGluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Texas-Austin, 2500
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 78)
Symonds, V.V. and Lloyd, A.M.
Analysis of Microsatellite Loci in Arabidopsis thaliana.
Mutational dynamics and application
Genetics 165 (3), 1475-1488 (2003)
                                                                                                                                                                         Arabidopsis thaliana Per-2 microsatellite nga8 sequence.
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113
7
0
0
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Mismatches:

    .78
    /note="microsatellite nga8"

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Matches:
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                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 78)
Symonds, V.V. and Lloyd, A.M.
Direct Submission
Submitted (08-MAX-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
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                                                                        GluGluGluArgArgLysGluIle 430
                                                                                                   GAGAGAGAGAGAGAGCATTA 6
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AY295846
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AY293995.1 GI:32478851
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52.00%
1.13%
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ACCESSION
VERSION
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VERSION
KEYWORDS
SOURCE
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TITLE
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REFERENCE
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PLN 11-DEC-2003
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 AlaGluGlnGluArgLysGluArgGluArgGlnGluGluGluAlaLysArgGlnLeuGlu 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
                                                                                                                                                                                              University of Texas-Austin, 2500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 LeuGluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluArg
1 (bases 1 to 90)
Symonds, V.V. and Lloyd, A.M.
An Analysis of Microsatellite Loci in Arabidopsis thaliana.
Mutational dynamics and application
Genetics 165 (3), 1475-1488 (2003)
14668396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Symonds, V.V. and Lloyd, A.W. M. Analysis of Microsatellite Loci in Arabidopsis thaliana. Mutational dynamics and application Genetics 165 (3), 1475-1488 (2003)
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Arabidopsis thaliana Ob-3 microsatellite nga8 sequence.
AY293994
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Mismatches:
Indels:
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Organism="Arabidopsis thaliana"

/mol type="ganomic DNA"

/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                      thaliana"
                                                                                                                                                                                                                                                                                                                                                 /ecotype="Pa-3"
1. .90
/note="microsatellite ngal72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="microsatellite nga8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                              2 (bases 1 to 90)
Symonds, V. V. and Lloyd, A.M.
Direct Submission
Submitted (11-MAY-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
1. 90
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Symonds, V.V. and Lloyd, A.M.
Direct Submission
Submitted (08-MAY-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                 /organism="Arabidopsis
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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	77	16	Ŋ	٣	17	г
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	8.85e+04	. 67.50	51.22%	39.02%	1.08%	8
Alignment Scores:			:	Best Local Similarity:		DB:

US-09-674-237B-3 (1-1213) x AY293994 (1-77)

601	27
390 GlnGluArgLysGluArgGluArgGlnGluGlnGluAlaLysArgGlnLeuGluLeuGlu 409	::: :::
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Search completed: April 29, 2005, 10:38:23 Job time : 12126 secs

Db 28 ------GAC Qy 430 Ile 430 Db 73 ATT 75

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                                                                                                                                                                                                                                                                         Human, S' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 18169; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 18169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A,
                                  ArgGluAlaAlaLysArgGlu 439
                                                                AGAGAAGAGAAGAGAGAA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression and secretion vectors
                                                                                                                                    AAC14094 standard; cDNA; 87 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0122487P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
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                                                                                                                                                                                                        06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               EP1033401-A2
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                                                                                                                                                                      AAC14094;
                                  433
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                                                                                                    RESULT 15
                                                                                                                    AAC14094/
ID AAC1
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392 ArglysGluArgGluArgGlnGluGluGluAlaLysArgGlnLeuGluLeuGluLysGln 411

Length: Matches: Conservative: Mismatches: Indels:

6.74e+04 65.50

52.63% 42.11% 1.04%

Percent Similarity: Best Local Similarity:

Score:

Query Match DB:

Gaps:

US-09-674-237B-3 (1-1213) x AAC14094 (1-87)

8 8 8

412 LeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGlu 429

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93

64 AAAGTAGGCATCTTCCCTATCTTGTTA

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABBR3999), a sequence having 65% sequence identity to (SI), (SI) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) caused by altered expression of human POSHL1 including disgnosing and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a single exon probe useful in examples of the printine, but is brand or sequence did not form part of the printed the protein control or the present sequence did not form part of the printed the protein control or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL -1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification, but is based on sequence information supplied to Derwent
Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene; Rho GTPase; signal transduction; gene expression; cancer; vaccine; gene therapy; transgenic; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 11; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Patent Office
                                                                                                                                                                                                                                                                                                                                                             2001WO-US000664
2001WO-US000665
                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000667
30-JAN-2001; 2001WO-US000668
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2001WO-US000670
                                                                                                                                                                                                                                                                             28-JAN-2002; 2002EP-00001165
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2001US-0328205P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-684061/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AEOM-) AEOMICA INC
                                                                                                                                                                   EP1239051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2001;
10-OCT-2001;
                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                                         11-SEP-2002
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G; 24 T; 0 U; 0 Other; 13 13 11 11 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-674-237B-3 (1-1213) x ABV89298 (1-96) Sequence 96 BP; 28 A; 16 C; 28 5.94e+04 67.50 70.00% 43.33% 1.08% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: .. So

Score:

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comprising several chimeric molecules, where each chimeric molecule has a self-coalescing element (SCE) which is fused, linked or associated with a molecule of interest, and where each SCE is capable of causing individual chimeric molecules to coalesce with other chimeric molecules into higher order aggregates under conditions favourable to aggregation. The aggregate is useful for treating or preventing a disease or condition in a patient and has a range of applications including therapeutic, prophylactic and chemical processes. The aggregate comprises a therapeutic polypeptide such as granulocyte-macrophage colony-stimulating factor (GM-CSF), useful for treating haematopoietic conditions such as myelosuppressive disorders e.g. AIDS, infectious diseases, autoimmune diseases, allergies, viral, bacterial and parasitic infections and cancers such as melanoma, leukaemia and lymphoma. This sequence represents DNA encoding an SCE peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated or purified higher order aggregate comprising several chimeric molecules having self-coalescing element associated or fused with molecule, useful in chemical, therapeutic and prophylactic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated or purified higher order aggregate
                                                                                                                                                                                    Self-coalescing element; SCE; granulating factor; GM-CSF; granulocyte-macrophage colony-stimulating factor; GM-CSF; haematopoietic condition; myelosuppressive disorder; AIDS; infectious disease; autoimmune diseases; allergy; viral infection; bacterial infection; nancer; melanoma; leukaemia; lymphoma; cytostatic; anti-HIV; immunosuppressive; antiallergic; antibacterial; virucide; antiparasitic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98 BP; 7 A; 38 C; 6 G; 47 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                   DNA #23.
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                                    BP.
                                                                                                                                                   Self-coalescing element (SCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2003; 2003WO-AU000667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2002; 2002US-0384878P
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66.00
85.19%
59.26%
1.05%
                                    ADJ36166 standard; DNA; 98
                                                                                                            22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCEG-) SCEGEN PTY LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-035460/03.
P-PSDB; ADJ36087.
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                            WO2003102187-A1
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                                                                         ADJ36166;
RESULT 14
ADJ36166/c
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comprising a nucleic acid of the invention. The cotton ESTB are useful as molecular taggs to isolate genes, to amportant reage to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes are associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to militate stresses encountered during seed germination. The ESTB additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecules are further useful for detecting the presence or quantity of a protein or mRNA and for detecting the presence or quantity of a protein or mRNA and for detecting the presence as epecifically claimed EST isolated from a cotton variety Nucotton338 gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 73 BP; 0 A; 37 C; 0 G; 36 T; 0 U; 0 Other;

13 6 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 3.3e + 0470.00 79.17% 54.17% 1.12% 13 Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Best Local Score:

US-09-674-237B-3 (1-1213) x ACN59545 (1-73)

409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428

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ACN61067 standard; cDNA; 76 BP. RESULT 12 ACN61067/c

ACN61067;

02-DEC-2004 (first entry)

Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-C11, SEQ:15848.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton318; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P

(DEIK/) DEIKMAN J. (FENG/) FENG P C C. (FINC/) FINCHER K L. (ZIEG/) ZIEGLER T E.

Fincher KL, Ziegler TE; Feng PCC, Deikman J,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 15848; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTS;
ACN45220-ACN63099). The ESTS were isolated from CDNA libraries generated
CC ACN45220-ACN63099). The ESTS were isolated from CDNA libraries generated
CC from prined or non-primed seeds from variety DPSOB, manuture seeds from
Variety COKer 312 Boswell 96 Field, and androecium tissue, gynoecium
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucottoni3B. The invention also relates to substantially purified
CC comprising an uncleic acid of the invention. The cotton ESTs are useful as
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC members of a particular gene family. The nucleic acid molecules may be
CC members of a particular gene family. The nucleic acid molecules may be
CC members of a particular gene family. The nucleic acid molecules are
CC used for isolating a variety of agronomically significant genes important in initiating and molecular
CC associated with plant growth, quality, yield, and could also serve as
CC inks in metabolic and catabolic pathways. The nucleic acid molecules are
CC during seed germination. The ESTS additionally enable the acquisition of
CC during seed germination. The ESTS additionally enable the acquisition of
CC during seed germination. The ESTS additionally enable the acquisition of
CC detecting the acquisition of molecular markers useful in breaching
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the expression a specifically of a protein by tissue printing.
CC sequence represents a specifically printing of a protein by tissue printing of a protein or present specification, but was obtained in electronic format directly from the patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 76 BP; 0 A; 38 C; 0 G; 38 T; 0 U; 0 Other;

76 113 6 0 0 Conservative: Mismatches: Indels: Length: Matches: 3.45e+04 70.00 79.17% 54.17% 1.12% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.:

US-09-674-237B-3 (1-1213) x ACN61067 (1-76)

409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428 쉽

ABV89298 standard; DNA; 96 15 GAGAGAGAGA RESULT 13 ABV89298 g 2×2×4×8×

429 GluileGluarg 432

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BP.

23-DEC-2002 (first entry)

ABV89298;

Human POSHL1 single exon probe SEQ ID NO 11.

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                                                                                           \mathbf{n}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 GluLeuGluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArg 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy;
cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the U patent office at segdata.uspto.gov/sequence.html?bocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 4801; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                             81
6
6
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lated nucleic acids and polypeptides, useful for treating e.g. leukemia, inflammation and immune
                                                                                                                                                                                    0 A; 41 C; 0 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-674-237B-3 (1-1213) x ACN59315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                       2.61e+04
73.00
76.92%
53.85%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GAGAGAGAGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 ArgLysGlulleGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI84741 standard; cDNA; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAO04810
                                                                                                                                                                                 Sequence 81 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200164835-A2
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI84741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA184741

AA184741

AA184741

AA18

XXX
AA18

XXX
AA18

XXX
AA18

AA28

AA28

AA38

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to 17880 cotton expressed sequence tags (ESTs; ACM45220-ANN63099). The ESTs were isolated from CDNA libraries generated from primed or non-primed seeds from variety DP508, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, develophing fibrare, carpel walls and septer from variety Nucotton318. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the
                                                                                                                                                                                                                                                                                                Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-C5, SEQ:14326
                                              directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                              BP; 37 A; 11 C; 50 G; 0 T; 0 U; 0 Other;
                                                                                                                                984 99
                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ziegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 14326; 34pp; English.
                                                                                                                                                                                                                                               US-09-674-237B-3 (1-1213) x AAI84741 (1-98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fincher KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-2000; 2000US-0255619P.
                                                                                                                                                                                                                                                                                                                                                433 ArgGluAlaAlaLys 437
                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                           3.2e+04
73.00
76.00%
56.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACNS9545 standard; cDNA; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 70 GAGAGCGCGGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deikman J, Feng PCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tags to map genes.
                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004123340-A1
                                                                                                                                                              Percent Similarity:
                                                                                                                Alignment Scores:
                                                                                Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN59545;
                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                 Best Local
                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN59545/
                                                                                                                                                 Score:
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polynucleotides into DNA containing organelles, e.g. nucleus, comprises a first, a second, and optionally, a third polynucleotide segment.
                                                                                                                                                                                                                                                                                                      New nucleic acid construct capable of high efficiency delivery of
                                                                                                                       nucleic acid construct; vaccine; nucleic acid recognition sequence;
                                                                                                      Peptide nucleic acid (PNA) recognition sequence SEQ ID NO:2.
433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
         ---GAGAGAGAGAGAGAGAGAGAGAG 2
                                                                                                                                                                                                                                                                                                                                          Example 1; Page 46; 46pp; English.
                                                   ВЪ
                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LID
                                                                                                                                                                                                                17-SEP-2002; 2002WO-IL000772.
                                                                                                                                                                                                                                  17-SEP-2001; 2001US-0322449P.
                                                                                                                       Kappa B motif; pGL3 vector;
DNA transformation; peptide
                                                 ACC69626 standard; DNA; 88
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                     WPI; 2003-371818/35.
                                                                                                                                          vaccination; ss.
                                                                                                                                                                            WO2003025195-A2
                                                                                      18-JUL-2003
                                                                                                                                                                                              27-MAR-2003
                                                                                                                                                            Synthetic.
                                                                     ACC69626;
                                                                                                                                                                                                                                                                    Reich Z;
                                          ò
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The present invention describes a nucleic acid construct. The nucleic acid construct comprises: (a) a first polynucleotide segment including at least one nucleic acid sequence element; and (b) a second polynucleotide segment encoding a polypeptide including a nucleic acid binding domain being capable of specifically binding the above nucleic acid sequence element, and a localisation signal for directing transport of the polypeptide into a DNA containing organelle such that when the nucleic acid construct is introduced into a cell, expression of the polypeptide from the second polynucleotide segment directs transport of the nucleic acid construct into the DNA containing organelle. The nucleic acid construct is useful in high efficiency delivery of polynucleotides into DNA containing organelles such as nucleus, chloroplast or mitochondria, and containing organelles such as nucleus, chloroplast or mitochondria, and so can enhance any DNA transformation approach, including DNA vaccination approaches designed for therapeutic purposes. The nucleic acid sequence may also be used to isolate novel genes encoding nucleic acid sequence. ig proteins. The present sequence represents a peptide nucleic acid recognition sequence, which is used in an example from the present invention binding

Sequence 88 BP; 1 A; 44 C; 2 G; 41 T; 0 U; 0 Other;

```
888
77
77
14
                     Conservative:
Mismatches:
      Length:
Matches:
                                     Indels:
                                               Gaps:
      1.79e+04
              77.00
72.73$
51.52$
1.23$
                              Similarity:
                      Percent Similarity:
Alignment Scores:
                                      Query Match:
                               Best Local
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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432

US-09-674-237B-3 (1-1213) x ACC69626 (1-88)

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Cotton, plant, EST; expressed sequence tag, transgenic plant, gynoecium, variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                  Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-N6-D1, SEQ:14096.
                      433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
                               Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 14096; 34pp; English.
                                                                                                                                                                                                                                                                                          Fincher KL,
                                                                                                                                                                                                                      12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                     14-DEC-2000; 2000US-0255619P.
                                                                    ACNS9315 standard; cDNA; 81
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                          Deikman J, Feng PCC,
                                                                                                                                                                                                                                                   DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIBGLER T E.
                                                                                                                                                                                                                                                                                                         WPI; 2004-479808/45.
                                                                                                                                                                       Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                 tags to map genes.
                                                                                                                                                                                       US2004123340-A1.
                                                                                                   02-DEC-2004
                                                                                                                                                                                                      24-JUN-2004
                                                                                   ACN59315;
                                                                                                                                                                                                                                                                  (FINC/)
                                                                                                                                                                                                                                                    (DEIK/)
                                                                                                                                                                                                                                                            FENG/)
                                                     RESULT 9
                                                             ACN59315,
                                                                            ð
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Gossypium hirsutum.

fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular isolated nucleic acid molecule that encodes a plant protein or its tags to map genes

Claim 1; SEQ ID NO 15706; 34pp; English

The invention relates to 17880 cotton expressed sequence tags (ESTS; ACN45220-ACN63099). The ESTS were isolated from cDNA libraries generated from parimed or non-primed seeds from variety DESOB, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septe from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes to mapers, to determine gene function and to determining whether genes are useful for isolate genetic regions, to isolate genes are members of a particular gene family. The nucleic acid molecules may be used for isolated genes are associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes in these tissues and/or other tissues.

Conference or quantity of a protein by tissue printing. The present sequence represents a specifically clant, and con a protein or mitigate is a protein or mit and molecular manter of a protein or man and a protein and molecular manter of a protein or man and a protein and molecular manter of a protein or man and a protein or man a specifically contact of a protein or man and a protein or mand a protein or mand a protein or mand and a protein or mand a protein or mand a protein or mand a prote cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 89 BP; 0 A; 45 C; 0 G; 44 T; 0 U; 0 Other;

Conservative: Mismatches: Length: Matches: Indels: 1.43e+04 79.00 72.73% 51.52% 1.26% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Best Local

US-09-674-237B-3 (1-1213) x ACN60925 (1-89)

413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432 셤

433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445

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ACN59554/ RESULT 7

ACN59554 standard; cDNA; 89 BP.

ACN59554;

(first entry) 02-DEC-2004 Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-F1, SEQ:14335.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton318; library LIB382; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Ziegler TE; Fincher KL, 2-DEC-2001; 2001US-00021323 14-DEC-2000; 2000US-0255619P Deikman J, Feng PCC, FINCHER K L. ZIEGLER T E. DEIKMAN J. FENG P C C. US2004123340-A1. 24-JUN-2004 (FINC/) (ZIEG/) DEIK/) FENG/)

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 14335; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACM45220-ACM63099). The ESTB were isolated from cDNA libraries generated
CC from primed seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibree, carpel walls and septa from variety
CC from primed seeds from variety broteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTB are useful as
molecular tags to isolate genetic regions, to isolate genes to members of a particular gene function and to determining whether genes are
members of a particular gene family. The nucleic acid molecules may be
cused for isolating a variety of agronomically significant genes
associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTS additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
comprises genetic and molecular mapping, and in cloning of agronomically
schemes, genetic and molecular mapping, and in cloning of agronomically
contents and elso permits the acquisition of molecules are further useful for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein by tissue printing. The cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 89 BP; 0 A; 44 C; 0 G; 45 T; 0 U; 0 Other;

89 7 7 7 1 1 1 1 Matches: Conservative: Mismatches: Length: Indels: 1.43e+04 79.00 72.73% 51.52% 1.26% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Best Local

US-09-674-237B-3 (1-1213) x ACN59554 (1-89)

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432

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117
48 T; 0 U; 1 Other;
                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                  Gaps:
A; 47 C; 0 G;
                                84.00
68.75%
53.12%
1.34%
0
                                        Percent Similarity:
Best Local Similarity:
Sequence 96 BP;
                 Alignment Scores:
                                                       Query Match
DB:
                          ..
0
                                  Score:
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(1-96)US-09-674-237B-3 (1-1213) x ACN59485

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                           433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArg 444
                                                                                                   ઠે
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36 GAGAGAGAGAGAGAGAGAGAGAGAGANAGAGA 1

ACN46027 standard; cDNA; 88 02-DEC-2004 ACN46027;

Cotton primed seed EST Clone ID: LIB3825-013-Q1-N6-D1, SEQ:808. (first entry)

Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DPSOB; library LIB3R25; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P

DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. DEIK/)

(FENG/) (FINC/) (ZIEG/)

Ziegler TE; Fincher KL, Deikman J, Feng PCC,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 808; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTB; ACN65220-ACN63099). The ESTB were isolated from cDNA libraries generated from primed or non-primed seeds from variety Debols, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septa from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be

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used for isolating a variety of agronomically significant genes
associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTs additionally enable the acquisition of
promocers and cis-regulatory elements which will be useful to express
gronomically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecular markers useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules are further useful for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein by tissue printing. The
present sequence represents a specifically claimed EST isolated from a
cotton variety pps08 primed seed cDNA library (LIB3825). The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=US20040123340
```

Sequence 88 BP; 0 A; 44 C; 0 G; 44 T; 0 U; 0 Other;

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88
117
7
5
                      Conservative:
Mismatches:
Indels:
       Length:
Matches:
1.42e+04
79.00
72.73$
51.52$
                                Best Local Similarity:
                       Percent Similarity:
Alignment Scores:
                                       Query Match:
DB:
         Pred. No.:
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(1-88)US-09-674-237B-3 (1-1213) x ACN46027 413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432

433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445

----GAGAGAGAGAGAGAGAGAGAGAG

ACN60925, RESULT 6

ACN60925 standard; cDNA; 89

ACN60925;

02-DEC-2004 (first entry)

Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-N6-B7, SEQ:15706.

Cotton, plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1

24-JUN-2004.

12-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P

DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. (DEIK/) FINC/) FENG/)

ZIEG/)

Fincher KL, Deikman J, Feng PCC,

Ziegler TE;

WPI; 2004-479808/45

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ACN59485/c

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Deikman J, Feng PCC, Fincher KL,
         12-DEC-2001; 2001US-00021323.
                14-DEC-2000; 2000US-0255619P.
                       (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                               WPI; 2004-479808/45
                                                                 tags to map genes.
   24-JUN-2004.
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Ziegler TE;

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular

Claim 1; SEQ ID NO 14338; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTE; ACN45220-ACN63099). The ESTE were isolated from cDNA libraries generated from primed or non-primed seeds from variety DPSOB, mature seeds from variety coker 312 Boswell 96 Field, and androecium tissue, gynoecium variety coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septa from variety coker 10 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septa from variety concretising a nucleic acid of the invention. The cotton ESTS are useful as molecular case function and to determining whether genes are comprishing a nucleic acid of the invention. The cotton ESTS are useful as molecular tags to isolate genetic regions, to isolate genes are molecular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes are useful as molecular and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination. The ESTS additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues.

CC during seed germination. The ESTS additionally enable the acquisition of promoters and cis-regulatory elements which will be useful for chemes, genetic and molecular mapping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or maker of present sequence represents a specifically claimed EST isolated from a cotton variety Mucronarially element distormed and molecular mapping, and in cloning of agronomically sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the brinted EST specification, but was obtained in electronic format directly from the equence to sequence in the prese

Claim 1; SEQ ID NO 14266; 34pp; English.

Sequence 99 BP; 0 A; 50 C; 0 G; 49 T; 0 U; 0 Other;

The invention relates to 17880 cotton expressed sequence tags (ESTs;
ACM 45220-ACN63099). The ESTS were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DPSDB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
C hucotton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTS are useful
c invention, and to transformed plants having a nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid molecules are
comprising a nucleic acid of the invention. The cotton ESTS are useful
c invention, and to transformed plants having a nucleic acid molecules may be
conserved to a particular gene family. The nucleic acid molecules may be
members of a particular gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes
associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
closed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTs additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
schemes, genetic and molecular mapping, and in cloning of agronomically
catematical genes in these tissues and conterned
also permits the acquisition of molecules are further useful for
detecting the expression level or pattern of a protein or makNA and for
detecting the presence or quantity of a protein by tissue printing. The part of the conterned and protein and protein

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	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	5.03e+03	89.00	72.738	51.52%	1.42%	13
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-09-674-237B-3 (1-1213) x ACN59557 (1-99)

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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133 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445

cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequata.uspto.gov/sequence.html?DocID=US20040123340

Cotton; plant; BST; expressed sequence tag; transgenic plant; gynoecium; variety Nocotton38; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss. Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-G3, SEQ:14266. New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular Fincher KL, Ziegler TE; BP. 12-DEC-2001; 2001US-00021323 14-DEC-2000; 2000US-0255619P ACN59485 standard; cDNA; 96 02-DEC-2004 (first entry) Deikman J, Feng PCC, DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. WPI; 2004-479808/45. Gossypium hirsutum. tags to map genes. US2004123340-A1. 24-JUN-2004. ACN59485; (FINC/) (ZIEG/) (DEIK/) FENG/

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number of oligonucleotides derived from an orthologue gene of a different outputs or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different corganism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different corganisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the organism species A and the organism species B is less than corganism species A and the organism species B is the level-of. The sequence homology of the genes other than the orthologue gene of the organism species A and the organism species B is the level-of. The organism species B and the organism species B is the level-of. The organism species B and the organism species B is the level-of. The organism species B and the organism species B is the level-of. The organism species B and the organism species B is the melting. The found value or the calculated value of the melting.

The oligonucleotide array is useful for measuring expression distribution of the orthologue gene in different organisms. The method is useful for comparing expression change of the orthologue gene in different organisms. The method is useful for medical agent administration and for comparing change of the function of the orthologue gene in different organisms. The oligonucleotide array has the orthologue gene in different organisms. The oligonucleotide array has two or more types of organism simultaneously. The oligonucleotide array is unproves reliability of measurement. This polynucleotide sequence represents a probe of a rat gene for comparison against a human gene used in the oligonucleotide array of the invention.
different organism immobilized on support
                                                               Disclosure; Page 16; 56pp; Japanese.
gene of
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Sequence 80 BP; 19 A; 15 C; 25 G; 21 T; 0 U; 0 Other;

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000088
       Length:
Matches:
Conservative:
                              Mismatches:
                                      Indels:
       1.84
155.00
100.00%
100.00%
2.47%
                               Similarity:
                      Percent Similarity:
Best Local Similari
Alignment Scores:
                                     Query Match:
DB:
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US-09-674-237B-3 (1-1213) x ADP49483 (1-80)

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940 AspMetTrpTrpPheGlyGluValGlnGlyGlnLysGlyTrpPheProLysSerTyrVal 959
                    61
           960 LysLeuileSerGlyPro 965
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AAACTCATTTCAGGGCCC 79

ABN38018 standard; DNA; 60 BP RESULT 2

(first entry) 15-JUL-2002 ABN38018;

Human spliced transcript detection oligonucleotide SEQ ID NO:10766.

Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss.

Homo sapiens

WO200210449-A2

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903

28-JUL-2000; 2000US-0221607P.

02-MAY-2001; 2001US-0287724P

(COMP-) COMPUGEN INC.

Faigler S; Mintz L, Mintz E, Wasserman A, Shoshan A,

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmentalspecific genes.

Example 1; SEQ ID NO 10766; 47pp; English

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or cannering the corresponding transcriptom, and in detecting RNA transcripts may also be used as specialised mini transcriptomes. The libraries may also be used as specialised mini there is to detect transcriptome under a particular biological or pathological state, and so allowing the detection of tissue continuous precific pathological condition; to detect or apathology-specific genes such as those genes only expressed in specific genes; and to detect RNA transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from the parinted specification, but was obtained in electronic format carethy from WIPO at ftp. wipo.int/pub/published_pct_sequences

Sequence 60 BP; 19 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 644 102.00 100.00% 100.00% 1.63% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.:

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US-09-674-237B-3 (1-1213) x ABN38018 (1-60)

745 AlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIleGlnProGlyAsp 763 ð

ACN59557 standard; cDNA; 99 ACN59557/c RESULT 3

BP.

ACN59557;

02-DEC-2004 (first entry)

Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-F4, SEQ:14338.

Cotton; plant; BST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton318; library LiB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1.

OM protein

Run on:

Sequence:

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Acn5955 Cotton gy
Acn5954 Cotton gy
Acn59315 Cotton gy
Aai84741 Human pol
Acn59545 Cotton gy
Abv89298 Human pol
Acj36166 Self-coal
Acj36166 Self-coal
Acj36166 Self-coal
Acj36166 Self-coal
Acj36166 Self-coal
Acj36166 Self-coal
Acj3616 Human gen
Ach70530 Human gen
Ach70530 Human gen
Ach70530 Human spl
Ach80288 Human spl
Ach80288 Human gel
Ach80288 Human gel
Ach80286 Candida a
Ach80288 Candida a
Acc56404 Oligonucl
Ach80288 Luman gen
Ach80280 Candida a
Acc56404 Oligonucl
Ach80288 Luman gen
Ach80280 Candida a
Acc56404 Oligonucl
Ach80288 Luman gen
Ach80280 Candida a
Acc56404 Oligonucl
Ach80288 Luman gen
Ach80288 Luman gen
Ach80280 Candida a
Acc65408 Oligonucl
Ach80288 Luman gen
Ach80280 Candida a
Acc65408 Oligonucl
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Ach59546 Cotton gy
Aai84826 Human pol
Adi60206 Rat cDNA
Adi36167 Self-coal
Ach88910 Human gen
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Aac65407 Oligonucl
Aag13526 Sequence
Aaz57144 Exemplary
Ach89206 Human gen
Aaq62559 Candida a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonuclectide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonuclectides derived from ortholog
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Abn57047 N
Abn54472 M
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ACN61067
ABV89298
ADJ36166
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ADS31416
AAT23132
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AAF18418
AAQ33612
ACN46043
ACN59546
AAI84826
AAI84826
AAI60206
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    (HITA ) HITACHI LID
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-Q-fcgn2_1/USF0 spool/18096/4237/runat_27042005 182121_2866/app_query.fasta_1.
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-LIGT=245_DCALLGGN=200_THR_SCORE=pct_-TRR_MIX=blooum62_-TRANS=human40.cdi
-MODE=LOCAL_-OUTFNT=pto_-NOFM-ext_-HERPSIZE=500_-MINLEN=0_-MALIGN=15
-WODE=LOCAL_-OUTFNT=pto_-NOFM-ext_-HERPSIZE=500_-MINLEN=0
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Maximum DB seq length: 100
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102
89
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79
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Result

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Total number

Searched:

1

OM protein

Run on:

Sequence:

Searched:

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GSS 09-MAY-2003
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KE464 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE464
CR256469 77-E01084
CK878552 SGF139924
CC909028 BJ02039804
CC9295974 ESTR84351
CC912202 BJ02039804
CV295974 ESTR844351
CK455729 92994 MA
CV459729 92994 MA
CV296344 ESTR84721
BE662207 B511d06. y
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CV296344 ESTR84721
BE662207 B511d06. y
CK599753 io89f03. y
CK999753 io89f03. y
CK999753 io89f03. y
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CK9022319 VVD0882C06
BF645175 NF033F01E
BR445175 NF033F01E
BR445175 NF033F01E
BR445175 NF033F01E
CR922319 VVD0882C0
CC912318 BU332840
CC912138 BU332840
CC912131 BU3030840
CC912131 BU3030840
CC912131 BU3030840
CC9121413 BU0302840
CC9013141 CK432141
BE317674 NF053E021
CC9013140 CC900377A0
CC907845 BJ02017A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/sex="Male"
                                                                        AU246145
CRB86842
CX459729
CV296344
BE662207
CB29207
CR999753
CR135046
                                                                                                                                                                                    CB922319
BF645175
BE402129
BQ607527
                                                                                                                                                                                                                                                            AI947161
CD487616
BE976171
CO912138
                                                                                                                                                                                                                                                                                                                                                                                                BE317674
CB918229
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                                                                                                                                                                                                                                                                                                                                   CV297044
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20907631
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                             C21938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="129 ola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC199586
CC199586.1 GI:30479626
GSS.
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CC199586
LOCUS
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   Command line parameters:
-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09674237/runat_27042005_182122_2888/app_query.fasta_1.1351
-Q=/cgn2_1/USPTO_spool/US09674237/runat_27042005_182122_2888/app_query.fasta_1.1351
-Q=/cgn2_1/USPTO_spool/US09674237/runat_27042005_182122_2888/app_query.fasta_1.1351
-UNITS=b1cs -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1cs -START=1 -RND=1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
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-USFR=US09674237_@CGN 1 1 5042_@runat_27042005_182122_2888 -NCPU=6 -ICPU=3
-NO_WAAP -LARAGEQUERY -NGE_GCORRES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -SCARDEO=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA589590 V149009.8
AV963382 AV963382
CK891128 SCP163390
CB262655 53 B8866-
AL821665 AL821665
AU250968 AU250968
AW691901 NF05E018
AW691216 NF061F12S
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AA589590 vl49c09.s
AV963382 AV963382
                                                                                 April 28, 2005, 22:12:55 ; Search time 8531 Seconds (without alignments) 5412.256 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                          MAQFPTPFGGSLDVWAITVE.....VGLFPSNYVKLTTDMDPSQQ 1213
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                           34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                               0.5
7.0
7.0
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AA589590
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CK891128
CB262655
AL821665
AU250968
AW691901
                                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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99 htc:

99 est2:

99 est4:

99 est6:

99 gss1:

99 gss2:
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Maximum DB seq length: 100
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Match 1
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122
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Database:

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Result Š.

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95.50
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Ciona intestinalis
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                    sequence:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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AV963382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae, Mus.
1 (bases 1 to 79)
Marxa,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="whole skin"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/lab host="sOLR (kanamycin resistant)"
/clone lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Irom in week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
                                                                                                                                                                                                                                                                                                                                                                                                                                          AA589590 Tratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:975568 3' similar to SW:YFJ4_YEAST P43603 HYPOTHETICAL 40.4
                                                                                                                                                                                                                                                                   210 proproAlaAlaGluTrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPhe 229
                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMMGE Consortium (info@image.llnl.gov) for further information. MGI:556296
   /cell_type="Bmbryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTlLxf"
/note="Vector: pGTlLxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HMMI Mouse BST Project
Unpublished (1996)
Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 revl ET from Amersham High quality sequence stop: 1. Location/Qualiflers
                                                                                                             944
                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                         230 AsnSerHisAspLysThrMetSerGlyHisLeu 240
                                                                                                                                                                                                                                                                                                                                                                    61 AACAGCCACGACAAACTATGAGTGGACACTTA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .79
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:10090"
'clone="IMAGE:975568"
                                                                                                                                                                                                                                    (1-94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                      US-09-674-237B-3 (1-1213) x CC199586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA589590
AA589590.1 GI:2402970
                                                                                                             0.00165
168.00
100.00%
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                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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AA589590
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                                                              DRIGIN
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1099 LysAsnProGlyGlyTrpTrpGluGlyGluLeuGlnAlaArgGlyLysLysArgGlnIje 1118
                                                                                                                                                         1002 AlaMetTyrThrTyrGluSerSerGluGlnGlyAspLeuThrPheGlnGlnGlyAspVal 1021
                                                                                                                                                                                                                                                                                                                                     AV963382 Nori Satch unpublished cDNA library, egg Ciona integrinalis cDNA clone cieg21112 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (Basea I to 99)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished (2000)
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                             61
                                                                                                                                                                            2 GCCATGTACACATACGAGAGTTCTGATCAAGGAGATTTAAAGTTTCAGCAAGGGGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /.organism="Ciona intestinalis"
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/tissue_type="whole animal"
/dev_stage="egg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AAGACAGAAGGTGGATGGTGGAGGGAAAATACAATGGAAAA----
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Conservative:
Mismatches:
Indels:
                 Matches:
Conservative:
Mismatches:
Indels:
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Fmail: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1119 GlyTrpPheProAlaAsnTyrValLys 1127
 Length:
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                                                                                                                          US-09-674-237B-3 (1-1213) x AA589590 (1-79)
                                                                                                                                                                                                                                AV963382.1 GI:19451681
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/LOCE=Welcitz MILZ-MUSCONS (-); Site 1: BCORI; Site 2: XhOI; CDNA library from Arabidopsis thaTiana, accession C24; seedling; Lambda ZAPII phage library was made at the Max-Planck-Institute of Molecular Plant Physiology, Golm, Germany and mass-excised at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites BCORI-XhOI; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity.

'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de)
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 bp mRNA linear EST 15-JUL-2002
ALS21665 N:130 Triticum aestivum cDNA clone AOS_N130_plate_42, mRNA
ALS21665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 GluArgGluArgGlnGluGluGluAlaLysArgGlnLeuGluLeuGluLysGlnLeuGlu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breeding Research
                                                                                                                                               ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Resear
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Bmail: weisshaa@mpiz-koeln.mpg.de
Insert Length: 98 Std Brror: 0.00
Plate: 15 row; G column: 11
Seq primer: pBl2; GGTGGCGGCCCTCTAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 LysGlnArgGluLeuGluArgGlnArgGluGluArg 426
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179
179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Mprzp767G1115Q"
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="GABI:600378"
/db xref="taxon:3702"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-674-237B-3 (1-1213) x CB262655 (1-98)
                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/ecotype="C24"
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EST.
                                                                                                                               Contact: Weisshaar B
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87.50
78.79%
57.58%
1.40%
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Query Match:
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AL821665
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                                 99 bp mRNA linear BST 09-MAR-2004
SGP163390 Atlantic salmon Ovaries cDNA library Salmo salar cDNA
CLONE KG4-0756, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 bp mRNA linear EST 06-NOV-2003
53-E8866-008-015-G11-pBl2 MPIZ-ADIS-008 Arabidopsis thaliana cDNA
clone MPIZP767G1115Q 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
(bases I to 98)
Schmid, K. J., Soerensen, T. R., Stracke, R., Torjek, O., Altmann, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Ovaries"
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/lab_host="XL 10-Gold"
/clone_lib="Atlantic salmon Ovaries cDNA library"
/note="Vector: pBluescript II SK (+) XR; Site_1: EcoRI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                             Expressed Sequence Tags from an Atlantic salmon ovaries cDNA
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bjorn Hoyheim
Department of Basic Sciences and Aquatic Medicine
Norwegian School of Veterinary Science
De Dex 8140 DEP, NO-0033 Oslo, Norway
Tel: 47 22 96 47 03
Pax: 47 22 96 47 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Salmo salar"
/mol_type="mRNA"
/db_xref="taxon:8030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-674-237B-3 (1-1213) x CK891128 (1-99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Bjorn.Hoyheim@veths.no.
Location/Qualifiers
                                                                                                                                                                                            Salmo salar (Atlantic salmon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="KG4-0756"
                                                                                                                                                 CK891128.1 GI:45320861
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Best Local Similarity:
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CB262655
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/clone_lib="ST"
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DEFINITION
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AW691901
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AU250968 ST Lolium multiflorum cDNA clone ST007E06-5, mRNA sequence.
AU250968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: sikeda67@jfsass.or.jp
contact:Tadashi Takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GlulysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
Pooideae; Triticeae; Triticum.
1 (bases 1 to 96)
Wilson,I., Beswick,R., Shepherd,S., Barker,G., Parker,J., Owen,P.,
Walson,I., Coghill,J., Holdsworth,M., Lenton,J., Shewry,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards, K.
A BBSRC-funded wheat EST resource for the academic community Unpublished (2002)
Contact: Barker G
Institute of Arable Crop Research
Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lolium multiflorum EST Project
Unpublished (2004)
Contact: Selishi Ikeda
Japan Grassland Farming Forage Seed Association (JFSA)
Forage Crop Research Institute (FCRI)
Higaslakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
                                                                                                                                                                                                                                   /db_xref="taxon:4565"
/clone="A05_N130_plate_42"
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/dev_stage="z_days_post_germination"
/clone_lib="N:130"
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17
6
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lolium multiflorum"
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/mol_type="mRNA"
/do xref="taxon:451"
/clone="ST007E06-5"

    .96
    /organism="Triticum aestivum"

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                                                                                                                                                                                                           /mol_type="mRNA"
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Best Local Similarity:
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Pred. No.:
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AUTHORS
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NFOSOBOLSTIFIO00 Developing stem Medicago truncatula cDNA clone NFOSOBOLST 5', mRNA sequence.
AW691901
AW691901.2 GI:11931888
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.B.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
Mupublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7566637.
                                                                                                                                                                                                            /mol type="mkNa"
/db xref="taxon:3880"
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/dev_stage="Pooled developmental"
/clone lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Barkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
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    433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArg 444
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: radixon@noble.org
Insert Length: 826 Std Error: 0.00
Plate: 050 row: E column: 01
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (barrel medic)
Medicago truncatula
                                                                                    Indels:
                                                                                                        Gaps:
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/Global Libe WRIZ-ADIS-02/"
// Anote="Vector: pSORT1; Site 1: Sall; Site 2: Not1; cDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-0C in the light/Uv; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall Not!, primer sites and orientation:

T7-Sall-CCACGCCCCG-5prime-cDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further
                                                                                                       CB256469 97 bp mRNA linear EST 06-NOV-2003 77-E010847-027-001-A17-spP2 MPIZ-ADIS-027 Arabidopsis thaliana cDNA clone MPIZp772A171Q 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Windiplantae; Streptophyta; Embryophyta; Tracheophyta;
Gpermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 97)
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polyworphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissha@mpiz-koeln.mpg.de
Insert Length: 97 Std Error: 0.00
Plate: 1 row: A column: 17
Seg primer: spP2; ATTTAGGTGACACTATAGAAGA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | db xref="GABI:593663"
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| clssue_type="whole plant"
| dev stage="adult plant"
| lab_host="B. coli TOP10"
| clone_lib="MPIZ-ADIS-027"
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Conservative:
Mismatches:
62 AGAGAGAGAGAGAGAGAGAGAGACAGAGAGAG 97
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/ecotype="Ei-2"
                                                                                                                                                                                                         CB256469.1 GI:32881242
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                                                                                                                                                                                                                                                                                                                                                         AW693216 97 bp mRNA linear EST 21-DEC-2000 NF061F12ST1F1000 Developing stem Medicago truncatula cDNA clone NF061F12ST 5', mRNA sequence.
                                                                                            413 GlulysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosida, eurosida I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                            414 LysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArgArg 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 97)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stāgē="Pooled developmental"
/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA 741: 580 221 7300
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 856 Std Error: 0.00
Plate: 061 row: F column: 12
Seq primer: TCACACAGGAAACACTATCAC.
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                                              US-09-674-237B-3 (1-1213) x AW691901 (1-97)
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/db_xref="taxon:3880"
/clone="NF061F12ST"
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SGP139924 Atlantic salmon Gills cDNA library Salmo salar CDNA clone G7-0868, mRNA sequence.
CKR78555.1 GI:45308186
EST.
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BJ020399B01 BJ02 Capsicum annuum CDNA 5', mRNA sequence.
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1 (bases 1 to Solanales; Solanaceae; Capsicum.

Song, W. Y., Jeon, W. B., Kim, K. S., Lee, H. H., Ko, M. K., Kim, Y. S., Hong, J. C. and Oh, B. J.

Generation of Hot Pepper (Capsicum annuum) ESTS (Express Sequence Trags) from Red Ripe Fruit (Song, et al.)
                                                                                                                                                                                                                                                                                                                                                                          Hoyheim,B.
Expressed Sequence Tags from an Atlantic salmon gills cDNA library
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                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="pre-smolt"
/lab_host="%L 10-Gold"
/clone lib="Atlantic salmon Gills cDNA library"
/note="Vector: pBluescript II SK (+) XR; Site_1: EcoRI;
Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
Contact: Bjorn Hoyheim
Contact: Bjorn Hoyheim
Department of Basic Sciences and Aquatic Medicine
Norwegian School of Veterinary Science
PO Box 8146 DEP, NO-0033 Oslo, Norway
Tel: 47 22 96 47 58
Fax: 47 22 96 
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Salmo salar
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Best Local Similarity:
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/mol type="mRNA"
/db _xref="texon:8384"
/db _xref="texon:8384"
/db _xref="texon:8384"
/dow stage="texilbud head (stage 28-30)"
/dev stage="texilbud head (stage 28-30)"
/lab_host="Bscherichia coli DH108."
/clone lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 50g of poly A+ RNĀ from tailbud head. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                               CR580027 CC-tailbud-head Xenopus tropicalis cDNA clone THdA040a23
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1 (bases 1 to 97)

1 (bases 1 to 97)

Sanger Xenopus tropicalis EST project 2001 (2004)
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TROPICALIS_SEQUENCE_ID: THGA040a23.qlkT7
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
Seq primer: T7.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                    Xenopus tropicalis (western clawed frog)
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Indels:
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
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DB:
                         Query Match:
DB:
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CR580027/c
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61

RESULT 12

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scores:
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DRIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CV295974 1inear EST 23-SEP-2004 STST84351 petunia floral development CDNA library Petunia x hybrida CDNA clone Petunia-DevA-6-F01 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dclark@mail.ifas.ufl.edu
Contact Dr. Clark (dclark@mail.ifas.ufl.edu) for clone information
Seq primer: T3 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petunia x hybrida
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamids, Solanales, Solanaceae, Petunia.
1 (bases 1 to 100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                    /note="Wector: pBluescript II SK(+)XR; Site_I: ECORI;
Site_2: XhoI; cDNA library was generated from red ripe
fruit pericarp using lambda Zap II phage vector. In vivo
excision was done with helper phage to generate subclone
in pBluescript II SK(+)XR] vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Boung-Jun Oh
Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1545 Fifield Hall, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGlnLeuGlu 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4072"
/tissue type="red pepper fruit pericarp"
/clone lib="BJ02"
                                                                                                                                                                                                                                                                                                                                                                                                                 16559
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Florida
Environmental Horticulture Department, 1
110670, Gainesville, FL 32611-0670, USA
Tel: 352-392-1831 x370
Fax: 352-392-3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Petunia x hybrida"
                                                                                                                                                                         /organism="Capsicum annuum"
                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
Contact: David Clark
UF floriculture Biotechnology Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petunia x hybrida EST collection
                                                               Tel: 82 62 607 2422
Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 039 row: B column: 01.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-674-237B-3 (1-1213) x CO909028 (1-90)
                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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68.57%
54.29%
1.37%
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Best Local Similarity:
Query Match:
                                                      Korea
                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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VERSION
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AUTHORS
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JOURNAL
COMMENT
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SOURCE
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/done="Petunia-Dav6-F01"
//issue_type="all floral organs"
//lab hoft="lambda ZAP1" unidirectional"
//lab hoft="lambda ZAP1" unidirectional"
//lone lib="petunia floral development cDNA library"
//one lib="petunia floral development cDNA library"
//note="Vector: pBluescript SK-; Site_1: EcoR1; Site_2:
Xhof; supplier: Petunia x hybrida cv. mitchell Diploid
plants were grown from seeds to a fully flowering stage
under standard greenhouse conditions. Ten entire flowers
of six developmental stages were collected on the same day
from plants grown in standard greenhouses. The flower
stages were as follows in chronological order from
youngest to oldest: stage 1 - no color in corolla;
o.5 inches long stage 2 - first sign of color in corolla;
corolla (not open); corolla 1.5 inches long stage 4 -
fully open corolla; anthers not yet dehisced stage 5 -
fully open corolla; freshly anthesed, bright yellowing of
corolla tube; dry brown pollen (if present); stigma dry.
Total RNA was extracted from each sample, and 100
micrograms of each sample was combined for subsequent poly
A+ mRNA selection and cDNA synthesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CO912202 90 bp mRNA linear EST 16-AUG-2004
BJ03029F05 BJ03 Capsicum annuum CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 GlnArgGluLeuGluArgGluArgGluGluGluArgArgLysGluIleGluArgArgGlu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Song,W.Y., Jeon,W.B., Kim,K.S., Lee,H.H., Ko,M.K., Kim,Y.S.,
Hong,J.C. and Oh,B.J.
Generation of Hot Pepper (Capsicum annuum) EST8 (Express Sequence
'cultivar="Mitchell Diploid (aka. Mitchell, aka W115 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamids, Solanales, Solanaceae, Capsicum.

    (bases 1 to 90)

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Matches:
Conservative:
Mismatches:
Indels:
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Unpublished (2004)
Contact: Boung-Jun Oh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-674-237B-3 (1-1213) x CV295974 (1-100)
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Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 029 row: F column: 0
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO912202
CO912202.1 GI:51302505
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86.00
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/note="Vector: DNA library was generated from red ripe fruit pericarp using lambda Zap II phage vector. In vivo excision was done with helper phage to generate subclone in pBluescript II SK(+) KR] vector."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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DB:
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Pred. No.:
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Search completed: April 29, 2005, 13:01:47 Job time : 8540 secs

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US-09-674-237B-3 (1-1213) x CO912202 (1-90)

15688, A 8, Appli 8, Appli 4, Appli 2841, Ap 13841, Ap 13841, Ap 13841, Ap 1360, A

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number Minimum DB Maximum DB

Searched:

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ERSULT.

1 US-09-281-481A-6/c

1 Sequence 6, Application US/09281481A

2 PATENT NO. 5818747

3 GENERAL INFORMATION:

APPLICANT: DAWKINS, ROGER L. and ABRAHAM, Lawrence J.

TITLE OF INVENTION: GENETIC ANALYSIS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: SCULLY SCOTT MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STREET: UNITS STATES OF AMERICA

STATE: NEW YORK

COUNTRY: UNITS STATES OF AMERICA

ZIP: 11530-0299

COUNTRY: UNITS STATES OF AMERICA

ZIP: 11530-0299

COUNTRY: TOW TOW MANAPINE

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Ploppy disk
                                                                                                                                                             US-09-580-923-14
US-09-866-108A-15688
US-08-136-277-8
US-08-479-403-8
US-08-835-734-8
US-09-59-894-4
US-08-956-171E-2841
                                                                                                                                                                                                                                                                                                                                  US-08-781-986A-2841
US-09-513-999C-13843
US-08-145-705A-3
US-09-513-999C-31160
US-09-461-697-229
US-08-222-177A-166
US-08-222-177A-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/281,481A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-182-175A-38
US-08-182-175A-42
US-08-182-175A-46
US-08-474-633A-35
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PCT-US92-06412-42
PCT-US92-06412-46
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US-08-823-771-35
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US-08-860-038-14
US-09-580-923-13
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/893,971
FILING DATE: 16-UTL-1997
APPLICATION NUMBER: US 232,229
FILING DATE: 29-APR-1994
APPLICATION NUMBER: PREST9 (AU)
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AU92/00583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/AU92/00583
FILING DATE: 30-OCT-1992
ATTORNEY/AGET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9279
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                       -MODEL-frame+_p2n.model_-DEV=x1h
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Sequence 7, Appli
Sequence 18169, A
Sequence 12952, A
Sequence 223, App
Sequence 28, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 1, Appli
                                                                                                                                                     April 29, 2005, 03:08:25; Search time 446 Seconds (without alignments) 4450.232 Million cell updates/sec
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Sequence
Sequence
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-281-481A-6
US-09-281-4B1A-7
US-09-281-4B1A-7
US-09-573-099C-18169
US-09-621-976-12952
US-09-621-976-12952
US-08-481-432-28
US-08-281-481A-5
US-08-145-705A-4
US-08-145-705A-3
US-08-145-705A-3
US-08-145-705A-3
US-08-182-175A-54
US-08-182-175A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                  , Xgapext
, Ygapext
, Fgapext
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6269
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Match
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Score

Result

Database :

65.5 65 64 64

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63.5 60 60 58 57 57

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single

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392 ArgLysGluArgGluArgGlnGluGlnGluAlaLysArgGlnLeuGluLeuGluLysGln 411
STRANDEDNESS: 811
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Roger L. and ABRAHAM, Lawrence J. TITLE OF INVENTION: GENETIC ANALYSIS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 22
CORRESPONDENCE ADDRESS: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: 11530-0239
COUNTRY: UNITED STATES OF AMERICA
ZIP: 11530-0239
COMPUTER READABLE FORM:
MEDIUM TYPE: FIORPY disk
COMPUTER: PR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCHILD RELEASE #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/281,481A
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118
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/893,971
FILING DATE: 03-APR-1994
APPLICATION NUMBER: PCT/AU92/00583
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AU92/00583
ATTORNEX/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REFERENCE/DOCKET NUMBER: 9279
TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 4346
INFORMATION FOR SEQ ID NO: 7: SEQUENCE TRANKERINGER, SEQ ID NO: 7: SEQUENCE TRANKER, SEQUENCE TRANKER,
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; Sequence 7, Application US/09281481A
Patent No. 6383747
; GENERAL INFORMATION:
                      TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
TELEPAX: +516 742 4366
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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88.00
76.67
60.00%
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Best Local Similarity:
Query Match:
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CLASSIFICATION:
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US-09-513-999C-18169/C

US-09-513-999C-18169/C

Sequence 18169, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REPERBINCE: 59.US2.REG

CURRENT FILING DATE: 1909-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 18169

LENTHH: 87

LENTHH: 87
                                                                                                                                                                                                                      413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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Matches:
Conservative:
Mismatches:
Indels:
                                                                length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                    US-09-674-237B-3 (1-1213) x US-09-281-481A-7 (1-96)
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65.50
52.63%
42.11%
1.04%
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US-09-513-999C-18169
                                                                  61.5
88.00
76.67%
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LOCATION: 14
OTHER INFORMATION: w=a
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LOCATION: 45
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; MOLECULE TYPE: DNA
US-09-281-481A-7
                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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| FALELIA NO. 22.7.9.4|
| FALELIA NO. 22.7.9.4|
| FALELIA NEUROSCIENCE, Inc. |
| APPLICANT: COGENT NEUROSCIENCE, Inc. |
| APPLICANT: Lo, Donald C. |
| APPLICANT: BATHEY, Shawn |
| APPLICANT: BATHEY, STUART D. |
| APPLICANT: PORTBURY, STUART D. |
| APPLICANT: FURDAMEN KAELUI |
| APPLICANT: FURDAMEN COMPOSITIONS AND METHODS FOR DIAGNOSING |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING |
| TITLE OF INVENTION: CELL DEATH |
| FILE REFERENCE: 10001-005-999 |
| CURRENT APPLICATION NUMBER: US/09/461,697 |
| CURRENT APPLICATION NUMBER: 1999-12-14 |
| NUMBER OF SEQ ID NOS: 466 |
| SEQ ID NO 223 |
| LENGTH: 96 |
                                                                                                        419 GluargGluargGluGluargargLysGluIleGluargArgGlualaAlaLysArg 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 LeuGluLeuGluLysGlnLeuGluLysGlnLysGlnLeuGluArgGlnArgGluGluGlu 425
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AMINO ACID SEQUENCES OF HYPERVARIABLE
REGION 1 OF THE ENVELOPE 2 GENE OF ISOLATES
OF HEPATITIS C VIRUS AND THE USE OF
REAGENTS DERIVED FROM THESE HYPERVARIABLE
SEQUENCES IN DIAGNOSTIC METHODS AND
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                                                                  US-09-674-237B-3 (1-1213) x US-09-621-976-12952 (1-82)
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Matches:
Conservative:
Mismatches:
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          Indel8:
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                                                                                                                                                                                                                                                                                                        Sequence 223, Application US/09461697
Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 28, Application US/08484322
; Patent No. 6110465
                                                                                                                                                                                   439 GluLeuGluArgGlnArg 444
                                                                                                                                                                                                                           65 AAGAAAGAGAGAAAGG 82
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64.00
82.14%
39.29%
          1.02%
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TITLE OF INVENTION: AMINITILE OF INVENTION: REGITITLE OF INVENTION: REAGITITLE OF INVENTION: REAGITITLE OF INVENTION: REAGITITLE OF INVENTION: SEQUITITLE OF INVENTION: VACCORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BUKH, J.,
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US-08-484-322-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
      Query Match:
DB:
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                                                                                                                                                                                                                                                                   N: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATH
30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia OTHER INFORMATION: ble and is often polymorphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 LysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGlu 429
                           52
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                                                                                       ----GAGAGAWWAAGAGAAAAGAGAGAAGAAAGAG 19
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APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
PILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
SUFFRENT OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12952
LENGTH: 82
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Matches:
Conservative:
Mismatches:
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Mismatches:
Length:
Matches:
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                                                                                                                                                                                                                                     APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC H
FILE REPERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12952, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                     RESULT 4
US-09-573-080A-449
Sequence 449, Application US/09573080A
Parent No. 6828097
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 449
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 69
                                                                                                    51
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APPLICATION NUMBER: US/09/281,481A
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APPLICATION NUMBER: German P (FILING DATE: October 30, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.57e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.00
83.33%
61.11%
0.96%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-281-481A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 ProProLeuAlaAsnGlyAlaProProValIleGlnProLeuProAlaPheAlaHisPro 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CCACCCATACATCTGGGGGCACCGCCGCATACAGCCTATGGCCTCACCAGCATCTTCA
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Sequence 5, Application US/09281481A
Patent No. 6383747
GENERAL INFORMATION:
APPLICANT: DAWKINS, Roger L. and ABRAHAM, Lawrence J.
TITLE OF INVENTION:
GENETIC ANDLYSIS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSES: SCULIX SCOTT
STREET: AGO GARDEN CITY PLAZA
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 Ala---AlaThrTrpProLysSerSerPhe 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-674-237B-3 (1-1213) x US-08-484-322-28 (1-96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GCCCTGGCGCCCGGCAGAAATCCAGCTCATTT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                   COUNTRY: USAR
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,322
FILLING DATE: JAME 7, 1995
CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/POCKET NUMBER: 36,459
REFERENCE/POCKET NUMBER: 36,469
TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA ZIP: 11530-0299
       MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.50
64.52%
54.84%
1.01%
ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-281-481A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIle 430
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STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: 10.5.A.
ZIP: 10591-5144
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: NEC PowerMate 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DARS:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: L'bberding, Antonius
TITLE OF INVENTION: SPECIFIC GENE PROBES AND
TITLE OF INVENTION: INVESTIGATION OF CANDIDA
TITLE OF INVENTION: ALBICANS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRING-HORN KRAMER & WOODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/893,971
FILING DATE: 16-UUL-1997
APPLICATION NUMBER: US 232,229
FILING DATE: 19-APR-1994
APPLICATION NUMBER: PK9279 (AU)
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AU92/00583
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REFERENCE/DOCKET NUMBER: 9279
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 4343
TELEPHONE: SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
LENGTH: 58 base pairs
LENGTH: SB base pairs
LENGTH: ALLOL ACID NO: 5:
CENTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08145705A
Patent No. 5489513
GENERAL INFORMATION:
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FELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                              score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage COMPUTER: NEC POWERMATE 1 Plus OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Springer, Wolfgang; Plempel, Manfred; APPLICANT: L bberding, Antonius TITLE OF INVENTION: SPECIFIC GENE PROBES AND TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC TITLE OF INVENTION: INVESTIGATION OF CANDIDA TITLE OF INVENTION: ALBICANS
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647 AspAlaGlnArgArgValGlnGluArgAspLysGln 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GAGGCCAAGAAGAAGGCAGAGAGGCCAAGAAGAAG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-674-237B-3 (1-1213) x US-08-145-705A-4 (1-100)
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APPLICATION NUMBER: German P 42 36 708.5
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
            REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
TELECOMMULTCATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPRAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SPRUNG HORN KRAMER & WOODS
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DAR.
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08145705A Patent No. 5489513 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Candida albicans
                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                   8.19e+03
                                                                                                                                   INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.00
75.00$
31.25$
0.96$
Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10591-5144
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HO
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                     US-08-145-705A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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90
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GENERAL INFORMATION:
APPLICANT: Saverio Carl Palco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P)
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ProProLeuValSerSerValPro-----ProAlaAlaValProProLeuAlaAsnGly 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 TGGCCT-----CTTCTGCCT------TCTTCTTGGCCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AlaProProValIleGlnProLeuProAlaPheAlaHisProAlaAlaThrTrpPro
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16
5
6
12
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Application US/08182175A Patent No. 5559223
                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                           Candida albicans
TELEPHONE: (914) 332-1700 TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                              1.16e+04
58.00
53.85%
41.03%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                 INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: E.I. d
STREET: 1007 Mark
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-182-175A-54/c
                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                              US-08-145-705A-3
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                                     TELEX:
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TELEPHONE:
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Pred. No.:
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                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                    OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                    OTHER
                                                                                                                                                                                                                                                                                                                                                                                       OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ProLeuValSerSerValProProAlaAlaValProProLeuAlaAsnGlyAlaProPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ccrrcarcrrcrcrrccarcrrcarcrrcrrcr
                                                                                                                                                                                                                                                            /function= "synthetic storage protein
/product= "protein"
                                                                                                                                                                                                                                                                                                                /standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-674-237B-3 (1-1213) x US-08-182-175A-54 (1-97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 ccarcacricarcircrecicares--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-474-633A-63/c
; Sequence 63, Application US/08474633A
; Patent No. 5773691
                                                                                                                                                                                                                                                                                                'gene= "ssp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C: SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 MARKET STREET
                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                       1.31e+04
57.00
47.50%
35.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CHIM
TITLE OF INVENTION: METH
TITLE OF INVENTION: NOT
TITLE OF INVENTION: AND
TITLE OF INVENTION: OF T
NUMBER OF SEQUENCE: 107
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                         STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                    FRATURE:
NAMEJ/KEY:
CDS
LOCATION: 2.88
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                     linear
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                                                                           TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ctrcarcrrctarccacarcacrrcarcrrct 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-674-237B-3 (1-1213) x US-08-474-633A-63 (1-97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                       function= "synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: E. I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                        /product= "protein"
/gene= "ssp"
/standard_name=
                                                                                                                                                                                                                                                                                                                                                          torage protein
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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 63, Application US/08823771 Patent No. 6459019 GENERAL INFORMATION:
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                                                                                                                          woulde
MOLECULE TYPE: DNA (genomic)
ORIGINAL SUNCE:
STRAIN
                                                        63:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.31e+04
57.00
47.50%
35.00%
0.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: E. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON STATE: DELAWARE
                                 TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                    E. coli
E: DHS alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPANY
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OTHER INFORMATION
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                                                                                                                                                                                                                                                                                                                                                        INFORMATION
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CLONE: 92-2
                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 cctarcace-------cctrcarcrictcrrccarccacrrcarcrictic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function= "synthetic storage protein
product= "protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene= "ssp"
/standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.
STREET: 1100 New YORK AVENUE, N.W.
               CURRENT APPLICATION DATA:
APPLICATION NUMBER:
PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION NUMBER: 97/743,006
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Azamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-7949
TELEFAX: (302) 892-7949
TELEFAX: 835420
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 ccarccacricarcricarcricarce
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   Microsoft Word, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.31e+04
57.00
47.50%
35.00%
0.91%
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: E. coli
                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2..88
OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
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STATE: D. C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity:
Query Match:
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CLONE: 92-2
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NAME/KEY: CDS
     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: State Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
CORRESPONDENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 ProLeuValSerSerValProProAlaAlaValProProLeuAlaAsnGlyAlaProPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ccrrcarcrrcrccrcca 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function= "synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                   ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30.684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEFAK: 302-992-4931
TELEFAK: 302-773-0164
TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-674-237B-3 (1-1213) x US-08-823-771-63 (1-97)
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [ndel8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "5.11.11.5"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US92-06412-54/c
; Sequence 54, Application PC/TUS9206412
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                     FILING DATE: <Unknown>
                                                                                                                                                                                                                                          LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                            STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 2..88
OTHER INFORMATION:
storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product= "protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.50%
35.00%
0.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene= "ssp"
                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: 92-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1007 Mark
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delaware
: USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
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8 셤 ò

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COMPUTER: IBM PC compatible
COREATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/32,766A
FILING DATE: 01-NOV-1994
FILING DATE: 10-NOV-1994
FILING DATE: 12-DEC-1993
ATTORNEY/AGENT INFORMATION:
RAPLICATION NUMBER: 25,323
ATTORNEY/AGENT INFORMATION:
TELEFRAMICATION INFORMATION:
TELEFRAMICATION INFORMATION:
TELEFRAMICATION NUMBER: 25,323
REPERRENCE/DOCKET NUMBER: 21,300
TELEFRAMICATION: 1020 861-3000
TELEFRAMICATION: 85 01-300
TELEFRAMICATION: 85 01-3000
TELEFRAMICATION: 85 01-3000
TELEFRAMICATION: 85 01-3000
TELEFRAMICATION: 86-1000
SECURIE TYPE: DNA (Genomic)
SEQUENCE CHARACTERISTICS: 11000
TYPE: 11000
SECURIE TYPE: DNA (Genomic)
SCORE: 10000
SCORE: 56-1000
SCORE: 56-1000
SCORE: 56-1000
SCORE: 56-1000
SCORE: 10000
SCORE: 100000
SCORE: 10000
SCORE: 1000
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US-09-674-237B-3 (1-1213) x US-08-332-766A-44 (1-85)

432 ArgArgGluAlaAlaLys 437

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:::|||::: 62 AAAAGGAAAGGAATGAAA 79 Search completed: April 29, 2005, 13:09:14 Job time : 449 secs

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 10766, Application US/09908975

Sequence 10766, Application US/09908975

Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi

APPLICANT: MINTZ, Liat

APPLICANT: M
                                                                                                                                                                                                                                  Sequence 808, App
Sequence 14335, A
Sequence 1506, A
Sequence 14096, A
Sequence 14096, A
Sequence 14326, A
Sequence 15848, A
Sequence 113, App
Sequence 449, App
Sequence 724, App
Sequence 724, App
Sequence 724, App
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Sequence 437, App
Sequence 824, App
Sequence 114, App
Sequence 114, App
Sequence 2210, A
Sequence 2210, A
Sequence 27220, A
Sequence 27220, A
Sequence 2795, A
Sequence 6, Appli
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Sequence 174, App
Sequence 8038, Ap
Sequence 22483, A
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                                                                                                                       Sequence 10766, A
                                                                                                                                                                                                 Sequence 14266, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Appl
Sequence 63, Appl
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                                                                                                               10.05-09-08-975-10766
10.05-09-08-975-10766
10.05-10-21-332-14338
10.5-10-021-332-14338
10.5-10-021-332-14335
10.5-10-021-332-14036
10.5-10-021-332-14096
10.5-10-021-332-14096
10.5-10-021-332-14096
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10.5-10-021-332-14331
10.5-10-021-333-184A-6
10.5-10-021-333-184311
10.5-10-021-333-184A-6
10.5-10-021
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US-10-015-535-8
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                                             Length
    Query
Match
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                                                                                                                       RESULT 1
    Result
No.
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-MODEL=frame+ p2n, model -DEV=x1h
-MODEL=frame+ p2n, model -DEV=x1h
-MODEL=frame+ p2n, model -DEV=x1h
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-Q=/cgn2 1/USFPG spool/US09674237/runat_27042005_182123_2929/app_query.fasta_1.1351
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-LOOPCLL=0 -LOOPEXT=0 -UNITS=bits -GRART=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAXELS=100
-MAXIEN=100 -USER=US09674237_@CGN 1 1 767 @runat_27042005_182123_2929 -NCPU=6
-ICPU=3 -NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPOR=10 - KGAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPOR=10 - DELUEXT=7
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3684.812 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQFPTPFGGSLDVWAITVE......VGLFPSNYVKLTTDMDPSQQ 1213
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1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/2/pubpna/Der_NEW PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/Der_NEW PUB.seq:*
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
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15: /cgn2_6/prodata/2/pubna/US10B
                                                                                                                                                                                                                                      April 29, 2005, 06:53:05; Search time 2004 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapext
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6269
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Xgapop 10.0 ,
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Fgapop 6.0 ,
Delop 6.0 ,
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Maximum DB seq length: 100
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Database :

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SUMMARIES

Score:

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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(52274)B FILE REFERENCE: 38-21(52274)B CURRENT PAPLICATION NUMBER: US/10/021,323 CURRENT FILING DATE: 2001-12-12 PRIOR APPLICATION NUMBER: US 60/255, 619 PRIOR FILING DATE: 2000-12-14 NUMBER OF SEQ ID NOS: 17880 SEQ ID NO 14266 LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Tincher, Karen L.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US 10/10/21,323
CURRENT FILING DATE: 2001-12-12
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 808
LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 GluLysGluArgGluLeuGluArgGluArgGluGluGluArgArgLysGluIleGluArg 432
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Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3829-031-Q6-N6-G3
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Matches:
Conservative:
Mismatches:
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; OTHER INFORMATION: Clone ID: LIB3825-013-Q1-N6-D1
US-10-021-323-808
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US-10-021-323-808/c
Sequence 808, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
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79.00
72.73%
51.52%
1.26%
                                                                                                                                                                     TYPE: DNA
ORGANISM: Gossypium hirsutum
FRATURE:
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84.00
68.75$
53.12$
1.34$
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Best Local Similarity:
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                                                                                                                                                                                                                         NAME/KEY: unsure LOCATION: (1)..(
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Pred. No.:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                              Gaps:
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Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Delkman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Gossypium hirsutum
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102.00
100.00%
100.00%
1.63%
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Fincher, Karen L.
Ziegler, Todd E.
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72.73%
51.52%
1.42%
                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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Query Match:
           SOFTWARE: Patentin
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                           SEQ ID NO 10766
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Sequence 2, Application US/10488936
Publication No. US20050026149A1
Publication No. US20050026149A1
GENERAL INFORMATION:
APPLICANT: Reich, Ziv
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS CAPABLE OF HIGH EFFICIENCY DELIVERY OF
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
FILE REFERENCE: 27579
CURRENT APPLICATION NUMBER: US/10/488,936
CURRENT APPLICATION NUMBER: 2004-03-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
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Publication No. US20040123340A1
Publication No. US20040123340A1
Publication No. US20040123340A1
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Faul C.C.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
                                                                                                                                                                                                                                                         413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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; OTHER INFORMATION: Peptide nucleic acid (PNA) recognition sequence
US-10-488-936-2
                                                                                                                                                                                                                                                                                                                                            433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
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Matches:
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Mismatches:
Indels:
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Mismatches:
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Matches:
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                                                             1,33e+03
79.00
72.73%
51.52%
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      US-10-021-323-15706
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Pred. No.:
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LENGTH: 88
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APPLICANT: Peng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
PRIOR FILING DATE: 2000-12-14
SEQ ID NO 14335
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Applicant: Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR PLING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 15706
LENGTH: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . OTHER INFORMATION: Clone ID: LIB3829-032-Q6-N6-F1
US-10-021-323-14335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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                                                                                                                                                                                       ; Sequence 14335, Application US/10021323; Publication No. US20040123340A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15706, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Delkman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.33e+03
79.00
72.73
51.52
1.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                        US-10-021-323-14335/c
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Sequence 15848, Application US/10021323

Sequence 15848, Application No. US20040123340A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Deliman, Jill
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: 105,10/21,323
CURRENT APPLICATION NUMBER: US 60/255, 619
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 18948

LENGTH: 76
                                             APPLICANT: Peikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Frog, Paul C.C.
APPLICANT: Jodd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US 10/10/21,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
FRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 14326
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428
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13
6
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113
6
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; OTHER INFORMATION: Clone ID: LIB3829-031-Q6-N6-C11
(S-10-021-323-15848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-674-237B-3 (1-1213) x US-10-021-323-14326 (1-73)
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: LIB3829-032-Q6-N6-C5
 Sequence 14326, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.52e+03
70.00
79.17%
54.17%
1.12%
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70.00
79.17%
54.17%
1.12%
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Gossypium hirsutum
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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Pred. No.:
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APPLICANT: BILEOL-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, TRP-PI
TITLE OF INVENTION: SPLICE VARIANTS THEREOF
FILE REFERENCE: D0144 NP
CURRENT APPLICATION NUMBER: US/10/153,244
CURRENT PILING DATE: 2002-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-20
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 335
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 24
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                      407 GlubeuGlubysGlnbeuGlubysGlnArgGlubeuGluArgGlnArgGluGluGluArg 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 GlnGluArgLysGluArgGluArgGlnGluGluAlaLysArgGlnLeuGluLeuGlu 409
                                                                                                                                                                                                                                                                                                                                                                                                                                           410 LysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArg 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-674-237B-3 (1-1213) x US-10-021-323-14096 (1-81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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US-10-021-323-14096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-674-237B-3 (1-1213) x US-10-153-244-24 (1-99)
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 14096
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/10153244
Publication No. US20030144191A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 ArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GAGAGAGAGAGAGAGA 4
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72.00
72.97%
43.24%
1.15%
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73.00
76.92%
53.85%
1.16%
                                                                                                               TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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Best Local Similarity:
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US-10-021-323-14326/c
                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                 Alignment Scores:
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DB:
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DB:
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TITLE OF INVENTION: Higher molecular weight entities and uses therefor
              FILE REFERENCE: 2385978
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
FRIOR APPLICATION NUMBER: USSN 60/384878
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
LENGTH: 98
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                     US-10-449-831A-113
                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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DB:
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                                                             409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428
                                                                                         96
113
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                US-09-674-237B-3 (1-1213) x US-10-021-323-15848 (1-76)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10061201; Publication No. US20030166229A1; GENERAL INPORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN: FILE REFERENCE: P80178
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR PLING DATE: 2002-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-01
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Acomica Sequence Listing Engine
SERIGTH: 96
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70.00%
43.33%
1.08%
                                                                                                                                                    429 GluileGluArg 432
                                                                                                                                                                                              15 GAGAGAGAGA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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US-09-854-867-449

Sequence 449, Application US/09854867

Sequence 449, Application US/09854867

Publication No. US20030224356A1

Publication No. US20030224356A1

Publication No. US2003024356A1

APPLICANT: DOMN, KNOLL H

APPLICANT: ROGAN, PETER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING CURRENT APPLICATION NUMBER: US/09/854,867

CURRENT APPLICATION NUMBER: US/09/854,867

CURRENT FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SEQ ID NO 449

LENGTH NO 449

LENGTH NO 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia OTHER INFORMATION: ble and is often polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 LysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluGluArgArgLysGlu 429
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Mismatches:
Indels:
     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                   US-09-674-237B-3 (1-1213) x US-10-449-831A-113 (1-98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-674-237B-3 (1-1213) x US-09-854-867-449 (1-69)
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Matches:
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                                                                                                                                                                                                                                             433 ArgGluAlaAlaLysArgGlu 439
                                                                                                                                                                                                                                                                               28 AGAGAGAGAGAGAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
1.23e+04
66.00
85.19$
59.26$
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65.00
78.26%
52.17%
1.04%
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                                       Percent Similarity:
Best Local Similarity:
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Query Match:
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1020 AspValile---ValValThrLysLysAspGlyAspTrpThrGlyThrValGlyAsp 1038

1039 LysSerGlyValPheProSerAsnTyrVal 1048

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64 AAAGTAGGCATCTTCCCTATCTTGTA

Sequence 113, Application US/10449831A Publication No. US20040029179A1 GENERAL INFORMATION: APPLICANT: Koentgen, Frank

RESULT 13 US-10-449-831A-113/c

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RESULT 15
US-10-786-970A-449
US-10-786-970A-449

Sequence 449, Application US/10786970A

Publication No. US20050064449A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
CURRENT APPLICATION NUMBER: US/10/786,970A

CURRENT ELING DATE: 2004-02-24

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 449

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in
OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia
CHER INFORMATION: ble and is often polymorphi
US-10-786-9708-449
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Length:
Matches:
Conservative:
Mismatches:
Indels:

9.52e+03 65.00 78.26% 52.17% 1.04%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Gaps:

Search completed: April 29, 2005, 13:42:45 Job time : 2007 secs

61 AGAGAGAGA 69